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OM protein - protein search, using sw model

Run on: March 7, 2003, 11:19:49 ; Search time 38 Seconds
(without alignments)
1213.282 Million cell updates/sec

Title: US-09-909-775-2

Perfect score: 1879

Sequence: 1 MFLSILVALCLWLHLGVR.....SPKKNIKTRSAQKRTNPKRV 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1879	100.0	346	21 AAB00193	Breast cancer prot
2	1879	100.0	346	22 AAB76853	Human lung tumour
3	1879	100.0	346	23 ABG61803	Prostate cancer-as
4	1879	100.0	346	23 AAU85508	Clone #19118 of lu
5	1879	100.0	346	23 AA014432	Human frizzled rel
6	1870	99.5	368	19 AAW73508	Human ATG-1639 pro
7	1865	99.3	346	22 AAB48183	Human FRAZZLED pol
8	1865	99.3	368	20 AAY03232	Full length sequen
9	1862	99.1	368	20 AAW86346	Human FRAZZLED pro
10	1850	98.5	347	20 AAY03231	Amino acid sequenc

11	1807	96.2	346	21 AAB23911	Bos taurus Frazzle
12	1765	93.9	372	20 AAB86347	Partial human FRAZ
13	1765	93.9	372	22 AAB48184	Partial amino acid
14	831	44.2	325	19 AAW41767	Human hsfz protein
15	831	44.2	325	19 AAW48694	Bovine growth-indu
16	831	44.2	325	20 AAY03233	Amino acid sequenc
17	830	44.2	323	19 AAW41768	Mouse hsfz protein
18	830	44.2	323	19 AAW41253	Mouse "frazzled" f
19	830	44.2	323	23 ABB57262	Mouse ischaemic co
20	828	44.1	325	19 AAW48695	Human growth-induc
21	828	44.1	325	19 AAW41254	Human "frazzled" f
22	824	43.9	325	20 AAY03229	Amino acid sequenc
23	824	43.9	325	21 AAB10281	Xenopus sp embryo
24	817.5	43.5	319	19 AAW48696	Xenopus growth-ind
25	816	43.4	318	19 AAW41251	Xenopus "frazzled"
26	812.5	43.2	171	23 ABP41377	Human ovarian anti
27	698.5	37.2	143	20 AAY48252	Human prostate can
28	621.5	33.1	261	19 AAW41766	Hamster BHKsfz pro
29	338.5	18.0	585	18 AAW31271	Human frizzled-5 p
30	319	17.0	694	18 AAW31267	Drosophila frizzle
31	318	16.9	694	22 ABB71797	Drosophila melanog
32	308	16.4	694	23 AAU74823	Human REPTR 6 prot
33	305	16.2	685	18 AAW31274	Mouse frizzled-8 p
34	300.5	16.0	647	21 AAB12117	Hydrophobic domain
35	298.5	15.9	572	18 AAW31273	Mouse frizzled-7 p
36	289	15.4	589	22 ABB71245	Drosophila melanog
37	282	15.0	581	22 AAB73308	Human frizzled fam
38	275	14.6	582	22 AAB73307	Mouse frizzled fam
39	265	14.1	540	21 AAY90903	Human frizzled-4 p
40	263.5	14.0	666	18 AAW31268	Mouse frizzled-3 p
41	262.5	14.0	338	20 AAY30157	Amino acid sequenc
42	262.5	14.0	468	22 ABB12060	Human Frizzled-3 h
43	262.5	14.0	666	20 AAY30156	Amino acid sequenc
44	255	13.6	537	18 AAW31270	Mouse frizzled-4 p
45	255	13.6	537	23 ABB57288	Mouse ischaemic co

ALIGNMENTS

RESULT 1

AAB00193
ID AAB00193 standard; Protein: 346 AA.

XX

AC AAB00193;

XX

DT 08-FEB-2001 (first entry)

XX

DE Breast cancer protein BCX2.

XX

KW Breast cancer; diagnosis; prognosis; detection; screening;

KW antibody; oestrogen receptor; anti-oestrogen; immune response;

KW lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCH1; BCN1; BCN2;

KW BCN5; BCQ2; BCX2; BCX3; BCA2; BCR2; BCJ7; BCY3; human.

XX

OS Homo sapiens.

XX

PN WO200055629-A2.

XX

PD 21-SEP-2000.

XX

PF 15-MAR-2000; 2000WO-US06952.

XX

PR 15-MAR-1999; 99US-0268865.

PR 12-NOV-1999; 99US-0439878.

PR 12-NOV-1999; 99US-0440370.

PR 15-NOV-1999; 99US-0440493.

PR 16-NOV-1999; 99US-0440676.

PR 16-NOV-1999; 99US-0440677.

PR 29-NOV-1999; 99US-0450810.

PR 02-DEC-1999; 99US-0453137.

XX 08-MAR-2000; 2000US-0453137.

Db 181 KVKPTLATYLSKNYSYVIAHAKAVQSGCNEVTTVDVKEIFKSSSPIPTQVPLTN 240
QY 241 SSCQCPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSIQWEERLQEQRTVQD 300
Db 241 SSCQCPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSIQWEERLQEQRTVQD 300
QY 301 KKTAGTSSNPPKPKGPPAPKPPASPKNKIKTRSAQKRTNPKRV 346
Db 301 KKTAGTSSNPPKPKGPPAPKPPASPKNKIKTRSAQKRTNPKRV 346
RESULT 3
ABG61803
ID ABG61803 standard; Protein: 346 AA.
AC ABG61803;
XX
DT 15-AUG-2002 (first entry)
XX
XX Prostate cancer-associated protein #4.
XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
OS Mammalia.
XX
PN - W0200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US32045.
XX
PR 13-OCT-2000; 2000US-0687576.
PR 08-DEC-2000; 2000US-0733288.
PR 08-DEC-2000; 2000US-0733742.
PR 24-JAN-2001; 2001US-263957P.
PR 16-MAR-2001; 2001US-276888P.
PR 06-APR-2001; 2001US-281922P.
PR 24-APR-2001; 2001US-286214P.
PR 30-APR-2001; 2001US-0847046.
PR 04-MAY-2001; 2001US-288589P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
XX WPI; 2002-471335/50.
DR N-PSDB; ABK92118.
XX
XX Detecting a prostate cancer-associated transcript in a cell in a
PT patient, useful for diagnosing prostate cancer (PC) or screening
PT modulators of PC, by determining if prostate cancer-associated genes
PT are expressed in a prostate tissue -
XX
XX Claim 27; Page 304-305; 436pp; English.
PS
XX The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridise to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in
CC prostate cancer and are derived from the tissues of various
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC ABG61800-ABG61944 represent prostate cancer-associated proteins.

XX
SQ Sequence 346 AA;
Query Match 100.0%; Score 1879; DB 23; Length 346;
Best Local Similarity 100.0%; Pred. No. 4.6e-176;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHSTQENAILAEQ 60
Db 1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHSTQENAILAEQ 60
QY 61 YEELVDVNCSAVLRFFFCAMYPACTLEFLHDPDKPKSCVQCRARDCEPLMKYNHWP 120
Db 61 YEELVDVNCSAVLRFFFCAMYPACTLEFLHDPDKPKSCVQCRARDCEPLMKYNHWP 120
QY 121 ESLACDELPHYDRGVCISPEAIVTDLPEDVKWIDITPDMVVOERPLDVCCKRLSPDRCKC 180
Db 121 ESLACDELPHYDRGVCISPEAIVTDLPEDVKWIDITPDMVVOERPLDVCCKRLSPDRCKC 180
QY 181 KVKPTLATYLSKNYSYVIAHAKAVQSGCNEVTTVDVKEIFKSSSPIPTQVPLTN 240
Db 181 KVKPTLATYLSKNYSYVIAHAKAVQSGCNEVTTVDVKEIFKSSSPIPTQVPLTN 240
QY 241 SSCQCPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSIQWEERLQEQRTVQD 300
Db 241 SSCQCPHILPHQDVLIMCYEWRSMMLLENCLVEKWRDQLSKRSIQWEERLQEQRTVQD 300
QY 301 KKTAGTSSNPPKPKGPPAPKPPASPKNKIKTRSAQKRTNPKRV 346
Db 301 KKTAGTSSNPPKPKGPPAPKPPASPKNKIKTRSAQKRTNPKRV 346
RESULT 4
AAU85508
ID AAU85508 standard; Protein: 346 AA.
XX
XX AAU85508;
XX
DT 21-MAY-2002 (first entry)
XX
XX Clone #19118 of lung tumour protein.
DE Lung tumour; cancer; T cell; immune response stimulator;
KW cytostatic.
XX
XX Homo sapiens.
OS
XX W0200204514-A2.
PN
XX
PD 17-JAN-2002.
XX
PF 10-JUL-2001; 2001WO-US22058.
XX
XX 11-JUL-2000; 2000US-0614124.
PR 29-AUG-2000; 2000US-0651563.
PR 08-SEP-2000; 2000US-0658824.
PR 26-SEP-2000; 2000US-0671325.
PR 08-OCT-2000; 2000US-0677419.
PR 30-OCT-2000; 2000US-0702705.
PR 13-DEC-2000; 2000US-0736457.
PR 03-MAY-2001; 2001US-0849626.
XX
XX (CORI-) CORIXA CORP.
PA
XX Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
PI Warnerakis M, Carter D, Fanger GR, Vedwick TS, Bangur CS;
PI McNabb A, Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;
XX WPI; 2002-164634/21.
DR N-PSDB; ABK38036.
XX
XX Novel polynucleotide encoding a lung tumour polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumour protein -

Example 1; SEQ ID No 329; 223pp; English.

The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for removing tumour cells from a biological sample. The polynucleotide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This is the amino acid sequence of a lung tumour associated protein, described in the method of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

[illegible]

RESULT 5	
AAOI4432	
ID	AAOI4432 standard; Protein; 346 AA.
XX	
XX	AAOI4432;
XX	
XX	03-MAY-2002 (first entry)
DT	
XX	Human frizzled related protein 4 (FRP-4).
DE	
XX	
KW	Human; phosphate homeostasis modulation; frizzled related protein-4;
KW	FRP-4; phosphate transportation; serum phosphate concentration;
KW	hypophosphataemia; phosphaturia; 1,25-dihydroxy vitamin D deficiency;
KW	osteomalacia; phosphate homeostasis related disease;
KW	x-linked hypophosphataemia; rickets; oncogenic osteomalacia;
KW	rhabdomyolysis; cardiomyopathy; tumoral calcinosis; renal failure;
KW	bone mineralisation.
XX	
XX	Homo sapiens.
XX	
PN	WO200205857-A2.
XX	
PD	24-JAN-2002.
XX	
PF	19-JUL-2001; 2001WO-US23014.

19-JUL-2000; 2000US-219365P.
12-JAN-2001; 2001US-261438P.
(GENZ) GENZYME CORP.
Schlavi S, Madden SL, Manavalan P, Levine M, De Beur SJ;
N-PSDB; AAL41901.
Modulating phosphate homeostasis in a subject, for alleviating the
oncogenic osteomalacia-associated symptoms, comprises altering the
activity of frizzled related protein-4 (FRP4) or a gene encoding FRP-4
polypeptide .
Disclosure; Fig 2; 5lpp; English.
The invention comprises a method for modulating phosphate homeostasis in
a subject. The method involves altering the activity of the frizzled
related protein-4 (FRP-4), or altering the expression of the FRP-4 gene.
Phosphate plays a critical role in many cellular processes essential to
normal functionality of the human body. Phosphate homeostasis is
primarily regulated by the kidney, largely through variation in renal
tubular re-absorption of phosphate. Alterations of the phosphate
transporting function of the kidney and subsequent disturbance of serum
phosphate concentration often lead to serious biochemical and clinical
problems. The method of the invention is useful for modulating phosphate
homeostasis in a subject. The method of the invention can be used to
alleviate oncogenic osteomalacia-associated symptoms (e.g.
hypophosphataemia, phosphaturia, low serum concentrations of 1,25-
dihydroxy vitamin D and osteomalacia). The method of the invention can
also be used to treat phosphate homeostasis-related diseases (e.g.
X-linked hypophosphataemia, rickets, oncogenic osteomalacia,
rhabdomyolysis, cardiomyopathy, tumoral calcinosis, renal failure and
bone mineralisation). The present amino acid sequence represents the
human frizzled related protein 4 (FRP-4).

Query Match	100.0%;	Score 1879;	DB 23;	Length 346;
Best Local Similarity	100.0%;	Pred. No. 4.6e-176;		
Matches 346;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MFLSILVCLWLHLGLGVRGAPCEAVRIPCMCRIMPWNITBPMNHLLHHSOENATLAEQ	60	
Dd	1	MFLSILVCLWLHLGLGVRGAPCEAVRIPCMCRIMPWNITBPMNHLLHHSOENATLAEQ	60	
Qy	61	YEELVDVNCSAVLRFFFCAYAPICTLEFLHDPKPKCSVCORADDCPEPLMKMYNHSWP	120	
Dd	61	YEELVDVNCSAVLRFFFCAYAPICTLEFLHDPKPKCSVCORADDCPEPLMKMYNHSWP	120	
Qy	121	ESLACDELPPYDVGVCISPEAIVTDLPEDKWIDITPDMVQERPLDVDCRRLSPDRCCK	180	
Dd	121	ESLACDELPPYDVGVCISPEAIVTDLPEDKWIDITPDMVQERPLDVDCRRLSPDRCCK	180	
Qy	181	KVKPTLATYLSKNYSVIIIAKAVORSNGENVTVVDVAKEIFKSSSPIBRTQVPLTN	240	
Dd	181	KVKPTLATYLSKNYSVIIIAKAVORSNGENVTVVDVAKEIFKSSSPIBRTQVPLTN	240	
Qy	241	SSCOCPHLPHQDYLIMCYEHRSMMLLENCLVEKWRDQLSKRSQTOWERLQEQRRTVQD	300	
Dd	241	SSCOCPHLPHQDYLIMCYEHRSMMLLENCLVEKWRDQLSKRSQTOWERLQEQRRTVQD	300	
Qy	301	KKKTAGRTSRNSNPCKPGKPAPKPSPKKNIKTRSAOKRTNPKRV	346	
Dd	301	KKKTAGRTSRNSNPCKPGKPAPKPSPKKNIKTRSAOKRTNPKRV	346	

RESULT 6 ✓
AAW73508
ID AAW73508 standard; Protein; 368 AA.
XX

AC AAW73508;
 XX 01-MAR-1999 (first entry)
 XX Human ATG-1639 protein.
 XX Human; ATG-1639 protein; secreted ligand; 7-Transmembrane receptor;
 KW heart disease; hypertension; cardiovascular disease; kidney disease;
 KW obesity; insulin resistance; diabetes; Central Nervous System disorder;
 KW therapy; sFRP-4; frizzled protein; frizzb.
 XX Homo sapiens.
 OS EP879881-A1.
 PN 25-NOV-1998.
 XX 27-OCT-1997; 97EP-0308556.
 XX 14-JUL-1997; 97US-0892083.
 PR 23-MAY-1997; 97US-0047626.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Hu E, Zhu Y;
 PI - WPI; 1998-596873/51.
 DR N-PSDB; AAV08951.
 XX New nucleic acid encoding ATG-1639, a human analogue of frizzled
 XX receptor ligand - useful for treatment, prevention and diagnosis of
 PT - e.g. cardiovascular disease, obesity, or kidney disease
 XX Claim 11; Page 21-22; 28pp; English.
 XX This sequence is the human ATG-1639 protein of the invention.
 CC ATG-1639 is related to human secreted ligands for 7-transmembrane
 CC receptors of the frizzled family and is homologous to xenopus laevis
 CC Frizb protein and murine sFRP-4. ATG-1639 polypeptides and
 CC polynucleotides are useful for diagnosing susceptibility to diseases by
 CC detecting mutations in the ATG-1639 gene using probes containing the
 CC ATG-1639 nucleotide sequence, and can diagnose diseases associated with
 CC ATG-1639 imbalance by determining ATG-1639 polypeptide expression levels.
 CC ATG-1639 polypeptides can be used to screen for ATG-1639 agonists and
 CC antagonists which can be used in treatment to activate or inhibit
 CC ATG-1639 activity. In addition to direct administration of antisense
 CC sequences to prevent expression, or ATG-1639 polypeptides to treat
 CC conditions associated with a lack of ATG-1639. Gene therapy may also be
 CC used to affect endogenous ATG-1639 expression. ATG-1639 antibodies are
 CC useful for inducing an immune response to immunise and prevent diseases,
 CC and for isolating ATG-1639 clones or purifying the polypeptides by
 CC affinity chromatography. ATG-1639 polypeptides can be administered
 CC directly or as a vaccine to inoculate against disease. Diseases
 CC diagnosed, prevented or treated include: heart disease; hypertension;
 CC cardiovascular diseases; kidney diseases; obesity; insulin resistance;
 CC diabetes and Central Nervous System (CNS) diseases. The ATG-1639
 CC polypeptide is also useful for mapping the gene to a chromosome, allowing
 CC gene inheritance to be studied through linkage analysis.
 XX Sequence 368 AA:
 SQ Query Match 99.5%; Score 1870; DB 19; Length 368;
 Best Local Similarity 99.4%; Pred. No. 3.8e-175;
 Matches 344; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MELSILVALCLMLHALGVGAPCEAVRIPMCRHMPWNTTRPNHLHSTQENAILAIED 60
 DB 23 MELSILVALCLMLHALGVGAPCEAVRIPMCRHMPWNTTRPNHLHSTQENAILAIED 82
 QY 61 YEELVDVNCASVLRFFFCYAPICITLFLHDPKCKSVQCORDDCEPLMKMYNHSWP 120
 DB 83 YEELVDVNCASVLRFFLCYAPICITLFLHDPKCKSVQCORDDCEPLMKMYNHSWP 142

QY 121 ESLACDELVDYDRGVCISPEAIVTDLPEDVKWIDITPDMMVOERPLDVCKRLSPDRCKC 180
 DB 143 ESLACDELVDYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVCKRLSPDRCKC 202
 QY 181 KVKPPTLATYLSKNYSYVIHAKIKAVQSGCNEVTTVDVKEIFKSSSPTPTQVPLTN 240
 DB 203 KVKPPTLATYLSKNYSYVIHAKIKAVQSGCNEVTTVDVKEIFKSSSPTPTQVPLTN 262
 QY 241 SSCQCPIILPHODVLMCYEWSRMMLLENCLVEKWRDOLSKRSIQWERLQORRTVOD 300
 DB 263 SSCQCPIILPHODVLMCYEWSRMMLLENCLVEKWRDOLSKRSIQWERLQORRTVOD 322
 QY 301 KKKTAGRTSRSNPPKPKGPPAPKPPASPKKNTKTRSAQKRTNPKRV 346
 DB 323 KKKTAGRTSRSNPPKPKGPPAPKPPASPKKNTKTRSAQKRTNPKRV 368
 RESULT 7
 AAB48183
 ID AAB48183 standard; Protein; 346 AA.
 XX AC AAB48183;
 XX DT 02-APR-2001 (first entry)
 XX DE Human FRAZZLED polypeptide.
 XX KW FRAZZLED; antiinflammatory; osteopathic; immunosuppressive; AIDS;
 KW antiarthritic; cerebroprotective; vasotropic; nephrotropic; antHIV;
 KW cytotatic; antiarteriosclerotic; nootropic; neuroprotective; vaccine;
 KW gene therapy; human.
 XX OS Homo sapiens.
 XX PW WO200075280-A2.
 XX PD 14-DEC-2000.
 XX PF 08-JUN-2000; 2000WO-US15814.
 XX PR 08-JUN-1999; 99US-0327869.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PI Lark MW, James IE, Kumar S;
 XX WPI; 2001-080596/09.
 DR N-PSDB; AAC84495.
 XX New FRAZZLED polynucleotides and polypeptides useful for treating or
 XX preventing e.g. acute and chronic inflammation, autoimmune disorders,
 XX bone and cartilage diseases, cancers, or Alzheimer's disease
 PS Claim 11; Page 11; 37pp; English.
 XX The invention provides a human FRAZZLED polypeptide. The FRAZZLED
 XX polynucleotides and polypeptides are useful for treating chronic and
 XX acute inflammation (e.g. arthritis, osteoarthritis and other osteopenic
 XX conditions), Paget's disease, septicemia, autoimmune diseases, infection,
 XX stroke, ischemia, acute respiratory disease syndrome, renal disorders,
 XX restenosis, brain injury, AIDS (acquired immunodeficiency syndrome),
 XX metabolic and other bone diseases, cancer (e.g. bone and cartilage
 XX cancers or tumors, lymphoproliferative disorders), atherosclerosis, and
 XX Alzheimer's disease. The polynucleotides may be used as hybridization
 XX probes for cDNA and genomic DNA, to isolate cDNA and genomic clones of
 XX other genes having high sequence similarity to the FRAZZLED gene, and for
 XX chromosome identification. The polypeptides may further be used as
 XX immunogens to produce antibodies immunospecific for the FRAZZLED
 XX polypeptides, as an immunological or vaccine formulation against the
 XX above cited diseases, in screening for agonists and antagonists of the
 XX FRAZZLED polypeptides, to configure assays for detecting the effect of
 XX adding compounds on the production of FRAZZLED mRNA and protein in cells,
 XX and to identify membrane bound or soluble ligand or receptors through

PF 23-APR-1998; 98EP-0303163.
XX 26-NOV-1997; 97US-0978981.
PR 22-MAY-1997; 97US-0047408.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX James I, Kumar S, Lark M;
PI WPI: 1999-047873/05.
XX N-PSDB: AAV80657.
DR New FRZB -related (FRAZZLED) polypeptide and polynucleotide - useful
XX as diagnostic reagents and for prevention and treatment of cancer,
PT Alzheimer's disease and AIDS
XX
PS Claim 11; Page 7-8; 25pp; English.
XX
CC The present sequence represents human FRAZZLED protein from the FRZB
CC family. The FRZB family controls signalling and developmental
CC patterning. FRAZZLED proteins and polynucleotides are useful for
CC diagnosing diseases related to over or underexpression of FRAZZLED
CC protein by identifying mutations in the FRAZZLED gene, or determining
CC FRAZZLED protein expression levels. FRAZZLED proteins can be used to
CC screen for agonists and antagonists which bind the FRAZZLED protein
CC by observing the binding, or stimulation or inhibition of FRAZZLED
CC activity. These can be used in treatment to activate (agonist) or
CC inhibit (antagonist) FRAZZLED activity, in addition to direct
CC administration of antisense sequences to prevent expression, or FRAZZLED
CC polynucleotides to treat conditions associated with a lack of FRAZZLED
CC protein. Gene therapy may also be used to affect endogenous FRAZZLED
CC protein production. FRAZZLED antibodies are useful for inducing an
CC immune response to immunise and prevent diseases, and for isolating
CC FRAZZLED clones or purifying the protein by affinity chromatography.
CC FRAZZLED proteins can be administered directly or as a vaccine to
CC inoculate against diseases. Diseases diagnosed, prevented or treated
CC include: chronic and acute inflammation, arthritis, osteoarthritis,
CC septicemia, autoimmune diseases, transplant rejection, graft versus
CC host disease, infection, stroke, ischaemia, acute respiratory disease
CC syndrome, renal disorders, restenosis, brain injury, AIDS and cancer.
XX
SQ Sequence 368 AA:
Query Match 99.1%; Score 1862; DB 20; Length 368;
Best Local Similarity 99.1%; Pred. No. 2.3e-174;
Matches 343; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MFLSILVALCLWLHLALGVGAPCEAVRTPMCRHMPWNITRPNHLHSHSTQENAILAIQ 60
DB 23 MFLSILVALCLWLHLALGVGAPCEAVRTPMCRHMPWNITRPNHLHSHSTQENAILAIQ 82
QY 61 YEELVDVNCASVLRFFFCAMYPACTLEFLHDPKPKSVQCORARDCCPLMKMNHNSWP 120
DB 83 YEEVDVNCASVLRFFLCAMYPACTLEFLHDPKPKSVQCORARDCCPLMKMNHNSWP 142
QY 121 ESLACDELVYDRGVCISPEAIVTDLPEVKWIDITPDMVMQERPLDVCRLSPDRCK 180
DB 143 ESLACDELVYDRGVCISPEAIVTDLPEVKWIDITPDMVMQERPLDVCRLSPDRCK 202
QY 181 KVKVPTLATYLSKNYSYVTHAKIKAVQSGCNEVTVDVKEIFKSSSPIPTQVPLTN 240
DB 203 KVKVPTLATYLSKNYSYVTHAKIKAVQSGCNEVTVDVKEIFKSSSPIPTQVPLTN 262
QY 241 SSCQCPHILPHODVLIMCYENSRMMLLENCLEVKWRDLSKRSIQWEERLOPQRTVOD 300
DB 263 SSCQCPHILPHODVLIMCYENSRMMLLENCLEVKWRDLSKRSIQWEERLOPQRTVOD 322
QY 301 KKKTAGRTSRNPAPKPGKPPAPKSPASPKKNIKTRSAQRTNPKRV 346
DB 323 KKKTAGRTSRNPAPKPGKTPAPKSPASPKKNIKTRSAQRTNPKRV 368
RESULT 10

AAAY03231
ID AAY03231 standard; Protein; 347 AA.
XX
AC AAY03231;
XX
DT 16-AUG-1999 (first entry)
XX
DE Amino acid sequence of the human frezzled-like protein.
XX
KW Human frezzled-like protein; HFLP; frezzled protein family;
KW differentiation-related disorder; agonist; antagonist; antibody;
KW haematopoiesis; wound healing; cancer; inflammatory disorder;
KW autoimmune disease; allergic reaction.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /note= "signal peptide"
FT Domain 20..347
FT Domain /note= "mature protein"
FT Domain 25..145
FT Domain /note= "frazzled domain"
XX
PN WO9909152-A1.
PD 25-FEB-1999.
XX
PF 11-AUG-1998; 98WO-US16701.
XX
PR 10-APR-1998; 98US-0081438.
PR 12-AUG-1997; 97US-0055715.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Olsen HS, Ruben SM;
XX
DR WPI: 1999-190159/16.
DR N-PSDB; AAX28655.
XX
PT New isolated human frezzled-like protein - used to develop products
PT for treating e.g. cancers, inflammatory and autoimmune diseases,
PT infectious diseases and allergic reactions
XX
PS Claim 1; Fig 1A-1B; 152pp; English.
XX
CC This is the amino acid sequence of the human frezzled-like
CC protein (HFLP), used in the method of the invention. It is a
CC member of the frezzled protein family. It is used in the detection
CC and treatment of differentiation-related disorders. In conditions
CC where HFLP is under-expressed, its agonist is involved in the
CC treatment. Antagonist and antibodies of HFLP are used in the
CC treatment of disorder where HFLP is over-expressed, e.g. the
CC regulation of haematopoiesis, and wound healing. HFLP products are
CC used to develop products for treating e.g. cancers, inflammatory
CC and autoimmune diseases, infectious diseases and allergic
CC reactions.
XX
SQ Sequence 347 AA:
Query Match 98.5%; Score 1850; DB 20; Length 347;
Best Local Similarity 99.4%; Pred. No. 3.3e-173;
Matches 341; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 SILVALCLWLHLALGVGAPCEAVRTPMCRHMPWNITRPNHLHSHSTQENAILAIQYEE 63
DB 5 SILVALCLWLHLALGVGAPCEAVRTPMCRHMPWNITRPNHLHSHSTQENAILAIQYEE 64
QY 64 LYDVNCSAVLRFFFCAMYPACTLEFLHDPKPKSVQCORARDCCPLMKMNHNSWPESL 123
DB 65 LYDVNCSAVLRFFLCAMYPACTLEFLHDPKPKSVQCORARDCCPLMKMNHNSWPESL 124
QY 124 ACDELVYDRGVCISPEAIVTDLPEVKWIDITPDMVMQERPLDVCRLSPDRCKKV 183

Db 125 ACDELPLYDGVGVCISPEAIVTDLPEVDKWDITPDMMVQERPLDVKRLSPDRCKKV 184
 QY 184 KPTLATYLSKNYSYVTHAKIKAVORSGCNEVTVVDVKEIFKSSSIPRTQVPLITNSSC 243
 Db 185 KPTLATYLSKNYSYVTHAKIKAVORSGCNEVTVVDVKEIFKSSSIPRTQVPLITNSSC 244
 QY 244 QCPHILPHODVLIMCYEWSRMMLLENCLVKEWRDQLSKRSIQWEERLQORRTVQDKK 303
 Db 245 QCPHILPHODVLIMCYEWSRMMLLENCLVKEWRDQLSKRSIQWEERLQORRTVQDKK 304
 QY 304 TAGTSSRSNPPKPKGPPAPKPKPKNIKTRSAQRTNPKRV 346
 Db 305 TAGTSSRSNPPKPKGTPAPKPKPKNIKTRSAQRTNPKRV 347

RESULT 11

AAB23911 standard; Protein; 346 AA.

AC AAB23911;

DT 17-JAN-2001 (first entry)

DE Bos taurus Frazzled protein SEQ ID NO:2.

XX Bovine; Bos taurus; frazzled protein; FRZB family; cytostatic; antiHIV;
 KW human immunodeficiency virus; nontropic; vasotropic; neuroprotective;
 KW antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW cerebroprotective; antiarteriosclerotic; osteopathic; ophthalmological;
 KW antipsoriatic; cartilage; bone morphogenesis; regulator; inflammation;
 KW arthritis; rheumatoid arthritis; osteoarthritis; septicaemia; stroke;
 KW autoimmune disease; transplant rejection; graft versus host disease;
 KW infection; ischaemia; renal disorder; restenosis; brain injury; AIDS;
 KW bone disease; osteoporosis; cancer; lymphoproliferative disorder;
 KW atherosclerosis; Alzheimer's disease; retinitis pigmentosa;
 KW macular degeneration; degenerative eye disease.

OS Bos taurus.

PN W0200055202-A1.

PD 21-SEP-2000.

PF 15-MAR-2000; 2000WO-US06820.

PR 18-MAR-1999; 99US-0125038.

PR 03-MAR-2000; 2000US-0519397.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX James IE, Lark MW, Testa TT;

XX WPI; 2000-638181/61.

DR N-PSDB; AAA99046.

PT Novel Bos taurus Frazzled polypeptides and nucleotides encoding them,
 PT useful for treating inflammation, arthritis, acquired immunodeficiency
 PT syndrome (AIDS) and Alzheimer's diseases.

XX Claim 2; Page 27; 29pp; English.

PS The present sequence represents bovine (Bos taurus) Frazzled protein
 CC which is a member of the FRZB family. The frazzled protein can have
 CC cytostatic, antiHIV (human immunodeficiency virus), nontropic,
 CC vasotropic, neuroprotective, antiinflammatory, antiarthritic,
 CC antirheumatic, immunosuppressive, cerebroprotective, osteopathic,
 CC antiarteriosclerotic, ophthalmological and antipsoriasis activities,
 CC and is a regulator of cartilage and bone morphogenesis. The frazzled
 CC polynucleotide and protein are useful for treating and preventing
 CC chronic and acute inflammation, arthritis, rheumatoid arthritis,
 CC osteoarthritis, septicaemia, autoimmune diseases (e.g. inflammatory

CC bowel disease, psoriasis), transplant rejection, graft versus host
 CC disease, infection, stroke, ischaemia, acute respiratory disease
 CC syndrome, renal disorder, restenosis, brain injury, AIDS, metabolic and
 CC other bone diseases (e.g. osteoporosis), cancer (e.g. lymphoproliferative
 CC disorders), atherosclerosis, Alzheimer's disease, retinitis pigmentosa,
 CC macular degeneration and other degenerative eye diseases. The protein
 CC is also useful to establish assays to predict oral absorption and
 CC pharmacokinetics in man and thus enhance compound and formulation design,
 CC and in screening assays. The polynucleotide is useful for recombinant
 CC production of the frazzled protein.

SQ Sequence 346 AA;

Query Match 96.2%; Score 1807; DB 21; Length 346;
 Best Local Similarity 95.9%; Pred. No. 5.5e-169;
 Matches 331; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 MFLSILVALCLWLHALGVGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
 Db 1 MLLSILTALCLWLRLALGVGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60

QY 61 YEELVDVNCSAVLRFPPFCAMYPACTLEFLHDPKPKSVCORARDCEPLMKMYNHSWP 120

Db 61 YEELVDVNCSAVLRFPPFCAMYPACTLEFLHDPKPKSVQCRARDCEPLMKMYNHSWP 120

QY 121 ESLACDELPLYDGVGVCISPEAIVTDLPEVDKWDITPDMMVQERPLDVKRLSPDRCKC 180

Db 121 ESLACDELPLYDGVGVCISPEAIVTDLPEVDKWDITPDMMVQERPLDVKRLSPDRCKC 180

QY 181 KVKVPTLATYLSKNYSYVTHAKIKAVORSGCNEVTVVDVKEIFKSSSIPRTQVPLITN 240

Db 181 KVKVPTLATYLSKNYSYVTHAKIKAVORSGCNEVTVVDVKEIFKSSSIPRTQVPLITN 240

QY 241 SSCOCPHILPHODVLIMCYEWSRMMLLENCLVKEWRDQLSKRSIQWEERLQORRTVQD 300

Db 241 SSCOCPHILPHODVLIMCYEWSRMMLLENCLVKEWRDQLSKRSIQWEERLQORRTVQD 300

QY 301 KKTAGTSSRSNPPKPKGPPAPKPKPKNIKTRSAQRTNPKR 345

Db 301 KKTAGTSSRSNAPKPKGPPAPKPKPKNIKARSAPKSTNPKQ 345

RESULT 12

AAB86347

ID AAB86347 standard; Protein; 372 AA.

AC AAB86347;

DT 15-MAR-1999 (first entry)

DE Partial human FRAZZLED protein.

XX Human; FRAZZLED protein; FRZB; chronic inflammation; acute inflammation;
 KW arthritis; osteoarthritis; septicaemia; autoimmune disease; cancer;
 KW transplant rejection; graft versus host disease; infection; stroke;
 KW ischaemia; acute respiratory disease syndrome; renal disorder;
 KW restenosis; brain injury; AIDS; cancer.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 19
 FT /label= unknown
 FT /note= "encoded by GAN"

XX EP887406-A2.

PN 30-DEC-1998.

XX 23-APR-1998; 98EP-0303163.

XX 26-NOV-1997; 97US-0978981.

PR 22-MAY-1997; 97US-0047408.


```
QY 120 PESLACDELPPVDRGVCISPEAIVTDLPEVKWIDITPDMVMQERPLDVKCKRLSPDRCK 179
Db 143 PESLACDELPPVDRGVCISPEAIVTDLPEVKWIDITPDMVMQERPLDVKCKRLSPDRCK 202
QY 180 CKVKRPTLATYLSKNYSYVIHAKIKAVQSGGNEVTVVDVKEIFKSSSPIPTQVPLIT 239
Db 203 CKVKRPTLATYLSKNYSYVIHAKIKAVQSGGNEVTVVDVKEIFKSSSPIPTQVPLIT 262
QY 240 NSSCQCCHILPHQDVLMICY--EWSRSMMLLENCLVEKWRDOLSKRSQWEERLQEQRTVQ 299
Db 263 NSSCQCCHILPHQDVLMICYEWSRSMMLLENCLVEKWRDOLSKRSQWEERLQEQRTVQ 322
QY 300 DKKKTAGRTSRNPPKPKGTPAPKPKSPKKNIKTR---SAQKRTNPKRV 346
Db 323 DKKKTAGRTSRNPPKPKGTPAPKPKSPKKNIKTRGRTPRKRTPNPKRV 372

RESULT 14
AAW41767
ID AAW41767 standard; Protein; 325 AA.
AC AAW41767;
XX
DT 28-SEP-1998 (first entry)
XX
DE Human hsfz protein.
XX
KW Human; nerve cell growth factor; hsfz protein; neuronal cell;
KW proliferation; differentiation factor.
XX
OS Homo sapiens.
XX
PN DE19702835-A1.
XX
PD 22-JAN-1998.
XX
PF 27-JAN-1997; 97DE-1002835.
XX
PR 09-JUL-1996; 96DE-1027631.
XX
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Deutsch U, Drexler JCA, Lottspeich F, Mayr T, Risau W;
PI Rohrer H;
XX
DR WPI: 1998-088096/09.
DR N-PSDB; AAV13101.
XX
PT New nucleic acid encoding protein that increases neuronal cell
PT proliferation - useful as nerve growth factor and for detection or
PT inhibition of differentiation factors
XX
PS Claim 5: Page 17; 27pp; German.
XX
CC This sequence represents the human hsfz protein. This protein is found to
CC increase the proliferation of neuronal cells. Such proteins can be used
CC as nerve cell growth factors and for the detection and/or inhibition of
CC differentiation factors, specifically those corresponding to the
CC Drosophila melanogaster wingless or mouse int-1 type.
XX
SQ Sequence 325 AA;
Query Match 44.2%; Score 831; DB 19; Length 325;
Best Local Similarity 50.8%; Pred. No. 4.3e-73;
Matches 164; Conservative 52; Mismatches 77; Indels 30; Gaps 8;
QY 3 LSLVALCLWLHUALGVGAPCAVRIKCRHHPWNITRMPNHLHSTQENAILAIEQYE 62
Db 16 LLALALCL-LRVP-CARAAACEPVRIPLCKSLPNWTKMPNHLHSTQDNAILATEQFE 73
QY 63 ELVDVNCASVLRFFFCAMVPICTLEFLHDPIKPCSVQCARDDCEPLMKMYNHSWPS 122
Db 74 GLLGTHCSPLLFLFCAMVPICTIDFQHEPIKPCSVGERARQGCEPILIKYRHSWPEN 133
```

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QY 123 LACDELPPVDRGVCISPEAIVT---DLPEVKWIDITPDMVMQERPLDVKCKRLSPDRCK 178
Db 134 LACEELPPVDRGVCISPEAIVTADGADFMDSS-----NGNCRGASSERC 178
QY 179 KCKVKRPTLATYLSKNYSYVIHAKIKAVQSGGNEVTVVDVKEIFKSS-SPIPTQVPL 237
Db 179 KCKPIRATQKTYFRNNYTVIRAKVKEI-KTKCHDVTAVVEKVEIKLSLVNIPROTVNL 237
QY 238 IYNSCQCCHILPHQDVLMICY--EWSRSMMLLENCLVEKWRDOLSKRSQWEERLQEQ 295
Db 238 YTSGGCLCPLNVEEYILMGYEDERSLLLVESIAEKKWKDRLGCKVKRMDMKLRLHIG 297
QY 296 RTVDQKKKTAGRTSR-----SNP 313
Db 298 LKSDSSNSDSTQSQKSGRNSNP 320

RESULT 15
AAW48694
ID AAW48694 standard; Protein; 325 AA.
XX
AC AAW48694;
XX
DT 04-SEP-1998 (first entry)
XX
DE Bovine growth-inducing protein Frzb sequence.
XX
KW Frzb; growth-inducing protein; bovine; human; Xenopus; cartilage;
KW bone; nerve; muscle; tumour; Wnt-expressing tumour; myodegeneration;
KW subglottic stenosis; chondromalacia patellae; osteoarthritis;
KW joint surface lesion; neurodegeneration; Alzheimer's disease;
KW osteodegeneration; angiogenesis; wound healing.
XX
OS Bos sp.
XX
FH Key Location/Qualifiers
FT Peptide 7..27
FT /note= "putative signal peptide"
FT Cleavage-site 32..33
FT /note= "putative signal peptide cleavage site"
FT Protein 33..325
FT /note= "mature peptide"
FT Domain 35..147
FT /note= "N-terminal domain"
FT Region 73..94
FT /note= "putative transmembrane region"
XX
PN W09816641-A1.
XX
PD 23-APR-1998.
XX
PF 08-OCT-1997; 97WO-US18362.
XX
PR 20-MAR-1997; 97US-0822333.
PR 11-OCT-1996; 96US-0729452.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Hoang B, Luyten FP, Moos M, Wang S;
XX
DR WPI: 1998-251288/22.
DR N-PSDB; AAV18253.
XX
PT New nucleic acid encoding human, bovine and Xenopus Frzb protein -
PT and related proteins, antibodies, peptide(s), vectors and
PT transformed cells, used to induce growth of cartilage, bone, nerve
PT and muscle, also for inhibiting Wnt-expressing tumours
XX
PS Claim 4; Fig 1; 66pp; English.
XX
CC This represents a bovine growth-inducing protein Frzb. Bovine, human
CC and Xenopus Frzb genes which are shown in AAV18253 to AAV18255 are
```

CC related to the frizzled gene in Drosophila. The corresponding bovine,
CC human and Xenopus Frzb protein sequences are shown in AAW48694 to
CC AAW48696. A recombinant construct containing a Frzb encoding nucleic acid
CC linked to a heterologous promoter in an expression vector can be used to
CC produce recombinant Frzb proteins. The Frzb proteins may be formulated
CC with fibrin glue, freeze-dried cartilage grafts or collagen (optionally
CC also cartilage progenitor cells, chondroblasts or chondrocytes). They
CC are coated on to, or mixed with, a (non-)resorbable matrix, or mixed with
CC a biodegradable polymer. They modulate activity of the growth factors
CC Wnt-1 to 8. The Frzb proteins induce skeletal morphogenesis, embryonic
CC pattern formation and tissue specificity and are used to induce growth
CC of cartilage, bone, nerve and muscle, particularly in cases of
CC subglottic stenosis, chondromalacia patellae, osteoarthritis, joint
CC surface lesions, neurodegeneration (e.g. Alzheimer's disease),
CC myodegeneration or osteodegeneration. They also modulate Wnt-mediated
CC signalling in cells, and are used to inhibit growth of Wnt-expressing
CC tumours (particularly mammary or intestinal). The Frzb genes may also be
CC used to identify specific modulators or as a growth factor for cells of
CC the chondrocyte lineage in vitro, to stimulate wound healing, to promote
CC angiogenesis, to prevent transplant rejection and as adjunct to
CC chemotherapy or immunotherapy. Fragments of Frzb proteins are used for
CC detecting genetic abnormalities associated with Frzb genes.

XX Sequence 325 AA:

Query Match 44.2%; Score 831; DB 19; Length 325;
Best Local Similarity 51.4%; Pred. NO. 4.3e-73;
Matches 166; Conservative 48; Mismatches 77; Indels 32; Gaps 8;

QY 3 LSLVALCLWLHLGVCAPCEAVRIPMCRHMPNITRMPNHLHSTQENAILATEQYE 62
DB 16 LLAALACL-LRVP-GARAAACEVRIPICKSLPNMTKMPNHLHSTQANAILATEQFE 73

QY 63 ELVDVNCSAVLRFFFCAMVAPICTLEFLHDPKCKVCORARDCEPLMKMKNHWPES 122
DB 74 GLLTCHCSPDLLFFLCAMVAPICTIDFQHEPKCKVCERARQCEPILIKYRHSWPES 133

QY 123 LACDELVPYDVGVCISPEAIVT----DLPEDYKWDITPDMVQBRPLDVCCKRLSPDRC 178
DB 134 LACEELPVYDVGVCISPEAIVTAGDAPMDSS-----NGNCRGASSERC 178

QY 179 KCKKVKPTLATYLSKNYSVTHAKTAVORSOCNEVTVVDVKEIFKSS-SPIPRQTQVPL 237
DB 179 KCKPVRAQTQKTYERNYVIRAKYKEI-KTKCHDVTAVVEVKEILKASLVNIPRETVAL 237

QY 238 ITNSSQCCHILPHODVLIMCY--EWSRSMLENCLEKVRDOLSKRSIOWEERLQOR 295
DB 238 YTSGLCPPLNWNVEYLIMGYEDEERSKLLVGEISIAEKWKDRLGKVKRWDMKLRHLG 297

QY 296 RTVQD-----KKKTAGTSRS 311
DB 298 LNTSDSHSDSTQSQKPGNSNS 320

Search completed: March 7, 2003, 11:23:56
Job time : 40 secs

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Result No.	Query			Length	DB	ID	Description
	Score	Match					
1	830	44.2	323	4	US-08-878-474-7	Sequence 7, Appli	
2	828	44.1	325	4	US-08-878-474-9	Sequence 9, Appli	
3	816	43.4	318	4	US-08-878-474-3	Sequence 3, Appli	
4	338.5	18.0	585	4	US-08-937-067-9	Sequence 9, Appli	
5	305	16.2	685	4	US-08-937-067-14	Sequence 14, Appli	
6	298.5	15.9	572	4	US-08-937-067-13	Sequence 13, Appli	
7	293	15.6	565	4	US-08-937-067-8	Sequence 8, Appli	
8	263.5	14.0	666	4	US-08-937-067-10	Sequence 10, Appli	
9	255	13.6	537	4	US-08-937-067-11	Sequence 11, Appli	
10	248	13.2	295	4	US-08-893-654B-6	Sequence 6, Appli	
11	232.5	12.4	281	4	US-08-893-654B-2	Sequence 2, Appli	
12	228.5	12.2	280	4	US-08-893-654B-4	Sequence 4, Appli	
13	228	12.1	314	4	US-08-937-067-7	Sequence 7, Appli	
14	220	11.7	706	2	US-08-987-289-2	Sequence 2, Appli	
15	218	11.6	295	4	US-08-937-067-2	Sequence 2, Appli	
16	215.5	11.5	709	4	US-08-937-067-12	Sequence 12, Appli	
17	207	11.0	317	4	US-08-937-067-6	Sequence 6, Appli	
18	199.5	10.6	212	4	US-08-937-067-4	Sequence 4, Appli	
19	149.5	8.0	641	4	US-09-233-989-10	Sequence 10, Appli	
20	110	5.9	787	2	US-08-720-484A-4	Sequence 4, Appli	
21	110	5.9	787	4	US-08-953-823A-4	Sequence 4, Appli	
22	110	5.9	787	4	US-09-398-239-4	Sequence 4, Appli	
23	107	5.7	793	2	US-08-720-484A-2	Sequence 2, Appli	
24	107	5.7	793	4	US-08-953-823A-2	Sequence 2, Appli	
25	107	5.7	793	4	US-09-293-505-16	Sequence 16, Appli	
26	107	5.7	793	4	US-09-293-505-17	Sequence 17, Appli	
27	107	5.7	793	4	US-09-398-239-2	Sequence 2, Appli	

[illegible]

RESULT 2

```

US-08-878-474-9
; Sequence 9, Application US/08878474
; Patent No. 6133232
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Bouwmeester, Tewis
; TITLE OF INVENTION: Endomeric, Cardiac and Neural Inducing
; TITLE OF INVENTION: Factors
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,474
; FILING DATE: 18-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,150
; FILING DATE: 20-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 3100.002US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/248-5500
; TELEFAX: 415/362-5418
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-878-474-9

```

Query Match 44.1%; Score 828; DB 4; Length 325;
Best Local Similarity 50.8%; Pred. No. 3.3e-74;
Matches 164; Conservative 51; Mismatches 78; Indels

QY 3 L5ILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTOENAILAEQYE 62

Db	16	LLALAALCL-LRYP-GARAAACBPVRIPLCKSLPWNNTKMPNHLIHUSTOANALLAEQEP	73
Qy	63	ELVDVNCASVLRFFFCAMTAPICLLEFLHDPICKPCKSVQCARDDCEPLMKYNNHSWPES	122
Db	74	GLLGTHCSPDLLEFLCAMVAPICTIDFQHEPIKPKCSVCERARQGCPEILIKYRHSWPN	133
Qy	123	LACDELPVYDRGVCISPEAIVT---DLPEDYKWIIDITPDMVQPERPLDVDCRKLSPDRC	178
Db	134	LACEELPVYDRGVCISPEAIVTAGDGADFPMDSS-----NGNCRGASSEHC	178
Qy	179	KCKVKPTLATYLSKNYSYVIHAKIRAVORSGCNEVTVVDVKEIPKSS-SP1PTQVPL	237
Db	179	KCAPIRATQKTYERNYNYVIRAKVEI-KTKCHDVTA VVEVKEILKSSLVN1PRDTVNL	237
Qy	238	ITNSSCOCPHILPHQDVLCINCY--ENRSRMMLLENCLVEKWRDOLSKRSIQWEERLOEQR	295
Db	238	YTSGCCUCLPNNYEYIIINGYEDEBSRLLLVVGSIAEKWKDRLGCKVKYKMDMKLRHLUG	297
Qy	296	RTVQDKKKTKTAGRTSR-----SNP	313
Db	298	LSKSDSNSSDSTOSOKSGRNSNP	320

RESULT 3

```

US-08-878-474-3
: Sequence 3, Application US/08878474
: Patent No. 613232
: GENERAL INFORMATION:
: APPLICANT: De Robertis, Edward M.
: APPLICANT: Bouwmeester, Tewis
: TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
: TITLE OF INVENTION: Factors
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESS: Majestic, Parsons, Siebert & Haue
: STREET: Four Embarcadero Center, Suite 1100
: CITY: San Francisco
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 94111-4106
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/878,474
: FILING DATE: 18-JUN-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/020,150
: FILING DATE: 20-JUN-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Siebert, J. Suzanne
: REGISTRATION NUMBER: 28,758
: REFERENCE/DOCKET NUMBER: 3100.002051
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/248-5500
: TELEFAX: 415/362-5418
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 318 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: PS-08-878-474-3

```

Query Match 43.4%; Score 816; DB 4; Length 318;
Best Local Similarity 50.3%; Pred. No. 5e-73;
Matches 161; Conservative 47; Mismatches 78; Indels

QY 22 APCEAVRIPCMCRHMPNNTITRMPNHLIHS"QENAILAEQYEEELVDVNCNSAVLRRFFCAMY 81

[illegible]

RESULT 4

```

US-08-937-067-9
: Sequence 9, Application US/08937067
: Patent No. 6433155
: GENERAL INFORMATION:
: APPLICANT: Umansky, Samuil
: APPLICANT: Melkonyan, Hovsep
: TITLE OF INVENTION: A FAMILY OF GENES ENCODING
: TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
: TITLE OF INVENTION: METHODS OF USE THEREOF
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/937,067

```

Query Match	18.0%	Score 338.5;	DE 4;	Length 585;
Best Local Similarity	33.3%	Pred. No. 3e-25;		
Matches 73; Conservative	37;	Mismatches 84;	Indels 25;	Gaps 6;

```

QY 64 LVDVNGSAVLRFFFCAYAPICTLEFLHDPIKCKSCVQQRADDCEPLAKMYHSHWPESL 123
   ||::||| || ||| :: ||::|||::| |||:| |||:
Db 73 LVEIQCSPOLRFFLCTMYTPICLPDY-HKPLPPCRSVCERAKAGCSPLMRQYGFAMPERM 131
   ||::||| || ||| :: ||::|||::| |||:| |||:
QY 124 ACDELPIYDVGVCISPEAIVTDLPEVDVKWIDITPDMWQERPL-----DVDCKRL 173
   ||||| ||||| ::|||::| |||::| |||:| |||:
Db 132 SCDRPLVIGR-----DAEVLCHMDYNRSEATTPRPFPAKPTLPGPGCAPASGGECPAG 185
   ||||| ||||| ::|||::| |||::| |||:| |||:
QY 174 SPDRCCKK-VKPTLATYLSKNYSYVIHAKIKAVQRSGC 211
   ||||| || ||| ::|||::| |||::| |||:| |||:
Db 186 GPFVCKCREPFPVIL-----KESHPLYNKVRTGQVPNC 218
   ||||| || ||| ::|||::| |||::| |||:| |||:

RESULT 5
US-08-937-067-14
; Sequence 14, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; APPLICANT: Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-937-067-14

```

Query Match	16.2%	Score	305;	DB	4;	Length	685;
Best Local Similarity	39.5%;	Pred. No.	7.9e-22;				
Matches	58;	Conservative	31;	Mismatches	46;	Indels	12;
						Gaps	5;

59	EQYEELVDVNC	SAVLFFFCAM	YAPICTE	LF	LD	PT	K	PK	CS	VQ	CR	AD	DC	E	P	L	M	K	M	N	H	S	118
60	EQYEELVDVNC	SAVLFFFCAM	YAPICTE	LF	LD	PT	K	PK	CS	VQ	CR	AD	DC	E	P	L	M	K	M	N	H	S	119
61	EQYEELVDVNC	SAVLFFFCAM	YAPICTE	LF	LD	PT	K	PK	CS	VQ	CR	AD	DC	E	P	L	M	K	M	N	H	S	120
62	EQYEELVDVNC	SAVLFFFCAM	YAPICTE	LF	LD	PT	K	PK	CS	VQ	CR	AD	DC	E	P	L	M	K	M	N	H	S	121
63	EQYEELVDVNC	SAVLFFFCAM	YAPICTE	LF	LD	PT	K	PK	CS	VQ	CR	AD	DC	E	P	L	M	K	M	N	H	S	122
64	EQYEELVDVNC	SAVLFFFCAM	YAPICTE	LF	LD	PT	K	PK	CS	VQ	CR	AD	DC	E	P	L	M	K	M	N	H	S	123
65	EQYEELVDVNC	SAVLFFFCAM	YAPICTE	LF	LD	PT	K	PK	CS	VQ	CR	AD	DC	E	P	L	M	K	M	N	H	S	124
66	EQYEELVDVNC	SAVLFFFCAM	YAPICTE	LF	LD	PT	K	PK	CS	VQ	CR	AD	DC	E	P	L	M	K	M	N	H	S	125
67	EQYEELVDVNC	SAVLFFFCAM	YAPICTE	LF	LD	PT	K	PK	CS	VQ	CR	AD	DC	E	P	L	M	K	M	N	H	S	126
68	EQYEELVDVNC	SAVLFFFCAM	YAPICTE	LF	LD	PT	K	PK	CS	VQ	CR	AD	DC	E	P	L	M	K	M	N	H	S	127
69	EQYEELVDVNC	SAVLFFFCAM	YAPICTE	LF	LD	PT	K	PK	CS	VQ	CR	AD	DC	E	P	L	M	K	M	N	H	S	128
70	HOEWPIE	QTSQ	DLK	FF	LC	S	M	T															

```

RESULT 7
US-08-937-067-8
; Sequence 8, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; APPLICANT: Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA

```

```

RESULT 8
US-08-937-067-10
: Sequence 10, Application US/08937067
: Patent No. 643155
: GENERAL INFORMATION:
:   APPLICANT: Umansky, Samuil
:   APPLICANT: Melkonyan, Hovsep
:   TITLE OF INVENTION: A FAMILY OF GENES ENCODING
:   TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES:
:   TITLE OF INVENTION: METHODS OF USE THEREOF
:   NUMBER OF SEQUENCES: 19
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: MORRISON & FOERSTER
:   STREET: 755 Page Mill Road
:   CITY: Palo Alto
:   STATE: CA
:   COUNTRY: USA
:   ZIP: 94304-1018
:   COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/937,067
:   FILING DATE:
:   CLASSIFICATION: 536
:   ATTORNEY/AGENT INFORMATION:
:   NAME: Lehnhardt, Susan K.

```



```

; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 666 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-937-067-10

Query Match 14.0%; Score 263.5; DB 4; Length 666;
Best Local Similarity 36.3%; Pred. No. 1e-17;
Matches 62; Conservative 30; Mismatches 52; Indels 27; Gaps 8;

QY 11 LW-LHLALVGRGA-----PCEAVRIPMCRHMPWNTITRMPNHLHSTQENAILATEQYEELV 65
Db 10 LWLLTVLQIGGHSLSFCEPITLRMCQQLPYNTTTPNPNLLNHYDQTAALAMEPEHPMV 69

QY 66 DVNCSAVLRAFFFCAMVAPICTLEFLDHPKPKSVCORADDCCEPLMKMYNHSWPESLAC 125
Db 70 NLDCSRDFRFFLCALYAPIC-MEYGRVTL-PCRRLICORAYSECSKLMEWFGVDPWEDMEC 127

QY 126 DELP-----VYDRGVCI-----SPEALVTD-----LPEDVKWIDITPDM 159
Db 128 SRFPDCEPYRLVLDNLVCDPTEGAPVAVORDYGFWCPELX---IDPDL 175

RESULT 9
US-08-937-067-11
; Sequence 11, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuel
; APPLICANT: Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 537 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-937-067-11
```

```

Query Match 13.6%; Score 255; DB 4; Length 537;
Best Local Similarity 27.2%; Pred. No. 5.2e-17;
Matches 69; Conservative 49; Mismatches 110; Indels 26; Gaps 7;

QY 3 LSLVALCLWLHLAGV---RGAPCEAVRIPMCRHMPWNTITRMPNHLHSTQENAILAIE 59
Db 21 LGLLLQFLLLRPTLGLFGDEEERRCDPIRTAMQNLGYNVTKRPNLVGHELOTDALQLT 80

QY 60 OYEELVDVNCSAVLRFFFCAMVAPICTLEFLDHPKPKSVCORADDCCEPLMKMYNHSW 119
Db 81 TFTPPLIQYGCSSQLQFLCSVIVPMCT-EKINIPICGCMGUSVYKRCRCEPVLRERGF 139

QY 120 PESLACDELPLYD--RGVCTISPEAIVTDLPEDVKWIDITPDMVQERPLDVCCKRLSPDR 177
Db 140 PDTLNCCKFPONDHNHMCMEGPG-----DEEVLPHKTPIQPGEE-----CHSVGSNS 188

QY 178 CKCKKVKPTLTYLSKNYSYVIHAKI-----KAVORSGCNEVTYVDVVKELFKSSSP 229
Db 189 DQYIWKRSINCLVLCGYDAGLYSRSAKETDIWMAVWASLC-FISTFTVLTLIDSSR 247

QY 230 IPTQVPLITNSSC 243
Db 248 FSYPERPIIFLSMC 261

RESULT 10
US-08-893-654B-6
; Sequence 6, Application US/08893654B
; Patent No. 6165748
; GENERAL INFORMATION:
; APPLICANT: RACIE, LISA, ET ALIA
; TITLE OF INVENTION: Frazzled NUCLEOTIDE SEQUENCES,
; TITLE OF INVENTION: EXPRESSION PRODUCTS, COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,654B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEINERT, M.C.
; REGISTRATION NUMBER: 31,544
; REFERENCE/DOCKET NUMBER: GI 5279
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498 8574
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-893-654B-6

Query Match 13.2%; Score 248; DB 4; Length 295;
Best Local Similarity 25.4%; Pred. No. 1.1e-16;
Matches 80; Conservative 48; Mismatches 109; Indels 78; Gaps 14;

QY 5 ILVALCLWLHLAGV-----GAPCEAVRIP-----MCRHMPWNTITRMPNHLHSTQEN 53
Db 13 LIVLLCF---LACGSSQWYLDFFGSSSRMRIPKSNALCYDYGSEMRIPLLHEHMAE 69
```


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OM protein - protein search, using sw model

Run on: March 7, 2003, 11:21:34 ; Search time 20 Seconds
(without alignments)
1663.126 Million cell updates/sec

Title: US-09-909-775-2
Perfect score: 1879
Sequence: 1 MFLSILVALCLWLHLALGVR.....SPKKNIKTRSAQRTNPKRV 346
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1033	55.0	197	JC7735	frizzled-related p
2	319	17.0	694	S71786	wingless receptor
3	300.5	16.0	647	JE0337	Frizzled-1 protein
4	300	16.0	641	A45054	probable intercell
5	298.5	15.9	574	JE0339	Frizzled-7 protein
6	293	15.6	565	JE0338	Frizzled-2 protein
7	289	15.4	581	S03540	gene frizzled prot
8	283	15.1	568	T25162	Frizzled-1 protein
9	282	15.0	581	JC7086	FZD10 protein - hu
10	279	14.8	550	T37325	wingless protein r
11	263	14.1	537	JC7127	frizzled protein 4
12	262.5	14.0	666	JC7312	frizzled-3 protein
13	226.5	12.1	605	T31690	hypothetical prote
14	220	11.7	706	JE0164	frizzled-6 protein
15	218	11.6	295	JE0174	frizzled protein-2
16	207	11.0	317	JE0175	frizzled protein-1
17	204	10.9	1113	JE0315	low-density lipopr
18	162	8.6	579	JC7629	membrane-type friz
19	149	7.9	1774	T3484	collagen alpha 1(X
20	120.5	6.4	526	T13484	frizzled protein h
21	107	5.7	400	T46383	hypothetical prote
22	107	5.7	3488	T34418	hypothetical prote
23	106.5	5.7	651	T21175	hypothetical prote
24	105	5.6	793	JC5539	Smoothed protein
25	103.5	5.5	965	S62935	hypothetical prote
26	98.5	5.2	492	F86384	probable protein f
27	96.5	5.1	581	B54665	netrin-2 precursor
28	96.5	5.1	1483	E80143	F6F3.12 protein -
29	94.5	5.0	606	A54665	netrin-1 precursor

30	94	5.0	859	2	T38168	hypothetical prote
31	94	5.0	6642	2	T29757	protein UNC-89 - c
32	92.5	4.9	1346	2	A57376	probable regulator
33	92	4.9	422	2	T39306	mitogen-activated
34	91.5	4.9	686	2	S70180	chemotaxis protein
35	91	4.8	1104	2	T38869	transcription fact
36	91	4.8	1151	1	S45390	protein kinase C (
37	91	4.8	1201	2	T29329	hypothetical prote
38	90.5	4.8	261	2	AB0337	probable Arac-fam
39	90.5	4.8	669	2	A35103	cell surface recep
40	90.5	4.8	960	2	JE0356	gamma-aminobutyric
41	90	4.8	591	2	T48141	acroganin - guine
42	90	4.8	1637	2	T00070	hypothetical prote
43	89.5	4.8	237	2	AH0207	Prop effector homo
44	89.5	4.8	497	2	T52308	very-long-chain fa
45	89.5	4.8	1030	2	T18374	B-cell receptor pr

ALIGNMENTS

RESULT 1
JC7735
frizzled-related protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 14-Dec-2001
C:Accession: JC7735
R:Yam, J.W.P.; Chan, K.W.; Wong, V.K.W.; Hsiao, W.L.W.
Biochem. Biophys. Res. Commun. 286, 94-100, 2001
A:Title: Transcriptional activity of the promoter region of rat frizzled-related prot
A:Reference number: JC7735; MUID:21378144; PMID:11485313
A:Accession: JC7735
A:Molecule type: DNA
A:Residues: 1-197 <YAM>
A:Cross-references: GB:AF140347
C:Comment: This protein is a new family of secreted proteins involved in tumorigenesi
C:Genetics:
A:Gene: rFrp
A:Introns: 148/3; 175/3

Query Match 55.0%; Score 1033; DB 2; Length 197;
Best Local Similarity 94.9%; Pred. No. 1.8e-76;
Matches 187; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY	1	MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHSTQENAILAIEQ	60
DB	1	MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHSTQENAILAIGQ	60
QY	61	YEELVDVNCSSVLRFFFCAMYPICITLFLHDPKPKSVQCARDDCEPLMKMYNHSWP	120
DB	61	YEELVDVNCSSVLRFFFCAMYPICITLFLHDPKPKSVQCARDDCEPLMKMYNHSWP	120
QY	121	ESLACDELVYDRGVCISPEAIVTDLPEDVKWIDITPDMVMQERPLDVCKRLSPDRCK	180
DB	121	ESLACDELVYDRGVCISPEAIVTDLPEDVKWIDITPDMVMQERPLDVCKRLSPDRCK	180
QY	181	KKVKPTATYLSKNYSY	197
DB	181	KKVKPTATYLSKNYSY	197

RESULT 2
S71786
wingless receptor precursor dfz2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 02-Mar-2001
C:Accession: S71786; S78444
R:Bhanot, P.; Brink, M.; Harryman Samos, C.; Hsieh, J.C.; Wang, Y.; Macke, J.P.; And
Nature 382, 225-230, 1996
A:Title: A new member of the frizzled family from Drosophila functions as a wingless
A:Reference number: S71786; MUID:96353971; PMID:8717036
A:Accession: S71786
A:Status: nucleic acid sequence not shown

A:Molecule type: DNA
A:Residues: 1-694 <BHA>
A:CROSS-references: EMBL:U65589
A:Note: mRNA was also sequenced
R:Bhanot, P.; Wang, Y.; Nathans, J.
submitted to the EMBL Data Library, July 1996
A:Reference number: S78444
A:Accession: S78444
A:Molecule type: DNA
A:Residues: 1-416, 'T', 418-694 <BHW>
A:CROSS-references: EMBL:U65589; NID:g1518050; PIDN:ACA47273.1; PID:g1518051
C:Gene: dfz2
A:CROSS-references: FlyBase:FBgn0016797
C:Superfamily: fruit fly frizzled protein
C:Keywords: transmembrane protein

Query Match 17.0%; Score 319; DB 2; Length 694;
Best Local Similarity 38.3%; Pred. No. 5.9e-18;
Matches 59; Conservative 25; Mismatches 40; Indels 30; Gaps 3;
QY 18 GVRGAP-----CEAVRIPCMRHPNITRMPNHLHSTQENAILAEQYEEELVDVNCSA 71
DB 52 GVPAIRDPNLRCEITIPMCRGIGTGMTSPFNMNHTQDEAGLEVHOFWPLVEIKSP 111
QY 72 VLRFEEFCAMYPACTLEFLHDPIKPKSVQCORARDCEPLMKMKNHNSWPESLACDELPPY 131
DB 112 DLAKFLCSMYTPIC-LEDYHKPLPVCRSVCCARSGCAPIMQYSFEPWPMACENLPLH 170
QY 132 DRGVCISPEAIVTDLPEYKVIDITPDMVMVOERP 165
DB 171 G-----DNDLCMEQP 181

RESULT 3
JE0337
Frizzled-1 protein - human
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
R:Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A:Title: Molecular cloning, differential expression, and chromosomal localization of
A:Reference number: JE0337; MUID:99032814; PMID:9813155
A:Accession: JE0337
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-647 <SAG>
A:CROSS-references: DDBJ:AB017363; NID:g3927882; PIDN:BAA34666.1; PID:g3927883
C:Superfamily: fruit fly frizzled protein

Query Match 16.0%; Score 300.5; DB 2; Length 647;
Best Local Similarity 45.2%; Pred. No. 1.7e-16;
Matches 52; Conservative 25; Mismatches 35; Indels 3; Gaps 2;
QY 24 CEAVRIPCMRHPNITRMPNHLHSTQENAILAEQYEEELVDVNCSAVLRFFFCAMYP 83
DB 116 CQIPISPLCTDIAYNOTIMPNLGHTNQDEAGLEVHOFPLVKVQCSAEKFLCSMYAP 175
QY 84 ICTLEFLHDPIKPKSVQCORARDCEPLMKMKNHNSWPESLACDELPPYDRG-VCI 137
DB 176 VCTV--LEQALPPCRSLCERARQGCCEALMNKFGQFWPDTLKCEKFPVHGAGELCV 228

RESULT 4
A45054
probable intercellular signal transducer or transmitter Fz-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 02-Mar-2001
A:Accession: A45054
R:Chan, S.D.; Karpf, D.B.; Fowlkes, M.E.; Hooks, M.; Bradley, M.S.; Vuong, V.; Bambino,
J. Biol. Chem. 267, 25202-25207, 1992
A:Title: Two homologs of the Drosophila polarity gene frizzled (fz) are widely expressed

A:Reference number: A45054; MUID:93094228; PMID:1334084
A:Accession: A45054
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-641 <CHA>
A:Experimental source: UMR 106 osteosarcoma cell line
A:Note: sequence extracted from NCBI backbone (NCBIP:120154)
C:Superfamily: fruit fly frizzled protein

Query Match 16.0%; Score 300; DB 2; Length 641;
Best Local Similarity 36.5%; Pred. No. 1.9e-16;
Matches 62; Conservative 26; Mismatches 38; Indels 44; Gaps 5;
QY 9 LCLWL---HLALGVRCAP-----CEAVR 28
DB 56 LLLNLLEAPLLGLVRAQAGQVSGPQORPPPPPOGGQOYNGERGISTPDHGYCOPIS 115
QY 29 IPMCRHPNITRMPNHLHSTQENAILAEQYEEELVDVNCSAVLRFFFCAMYPACTLE 88
DB 116 IPLCTDIAYNOTIMPNLGHTNQDEAGLEVHOFPLVKVQCSAEKFLCSMYAPVCTV- 174
QY 89 FLHDPIKPKSVQCORARDCEPLMKMKNHNSWPESLACDELPPYDRG-VCI 137
DB 175 -LEQALPPCRSLCERARQ-GCEALMNKFGQFWPDTLKCEKFPVHGAGELCV 222

RESULT 5
JE0339
Frizzled-7 protein - human
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C:Accession: JE0339
R:Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A:Title: Molecular cloning, differential expression, and chromosomal localization of
A:Reference number: JE0337; MUID:99032814; PMID:9813155
A:Accession: JE0339
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-574 <SAG>
A:CROSS-references: DDBJ:AB017365; NID:g3927886; PIDN:BAA34668.1; PID:g3927887
C:Superfamily: fruit fly frizzled protein

Query Match 15.9%; Score 298.5; DB 2; Length 574;
Best Local Similarity 46.1%; Pred. No. 2.2e-16;
Matches 53; Conservative 21; Mismatches 38; Indels 3; Gaps 2;
QY 24 CEAVRIPCMRHPNITRMPNHLHSTQENAILAEQYEEELVDVNCSAVLRFFFCAMYP 83
DB 49 CQIPISPLCTDIAYNOTIMPNLGHTNQDEAGLEVHOFPLVKVQCSPELRFLLCSMYAP 108
QY 84 ICTLEFLHDPIKPKSVQCORARDCEPLMKMKNHNSWPESLACDELPPYDRG-VCI 137
DB 109 VCTV--LDQAIPPCSLCERARQGCCEALMNKFGQFWPDTLKCEKFPVHGAGELCV 161

RESULT 6
JE0338
Frizzled-2 protein - human
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C:Accession: JE0338
R:Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A:Title: Molecular cloning, differential expression, and chromosomal localization of
A:Reference number: JE0337; MUID:99032814; PMID:9813155
A:Accession: JE0338
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-565 <SAG>
A:CROSS-references: DDBJ:AB017364; NID:g3927884; PIDN:BAA34667.1; PID:g3927885
C:Superfamily: fruit fly frizzled protein

RESULT 10

T37325

wingless protein receptor Cfz2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Mar-2001

C:Accession: T37325

R:Sato, A.; Kojima, T.; Uti-Tel, K.; Miyata, Y.; Saigo, K.

Development 126, 4421-4430, 1999

A:Title: Dfrizzled-3, a new Drosophila Wnt receptor, acting as an attenuator of Wingless

A:Reference number: Z21688; PMID:10498678

A:Accession: T37325

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-550 <SAT>

A:Cross-references: EMBL:AB026113; NID:g5931529; PIDN:BAA84678.1; PID:g5931530

C:Genetics:

A:Gene: Cfz2

C:Superfamily: fruit fly frizzled protein

C:Keywords: receptor; signal transduction; transmembrane protein

Query Match 14.8%; Score 279; DB 2; Length 550;

Best Local Similarity 30.7%; Pred. No. 7.9e-15;

Matches 75; Conservative 32; Mismatches 89; Indels 48; Gaps 9;

QY 1 MFLSILVALCLWLHLALGVGCA-----PCEAVRIPMCRHMPNITRMPNHLHSTQENA 54

DQ 1 MLLRISV-----LFLLLSGCALFGKQKCEQITPLCKGIGNWTSFNSYCHEKEEFA 55

QY 55 ILAIEQYBELVDVNCASVLRFFFCAMVAPICTLEFLHDPKCKSVQCORARDCEPLMKM 114

DQ 56 GLEVHGFYPLVEVGCFOHLKFFELCTWYTPICQ-ENYDKPILPCOMELCVARSKCSPIMAK 114

QY 115 YNHSWPESLACDELPE-----VYDRGVCISPEAIVTDLP-----EDVKW 152

DQ 115 YGRWNPETLSCEALPKMDOMSTGNICAAAP---PDPKQKHGHKKNONQNNHNY 170

QY 153 IDITPMVMQERPLDVKRLSDRCKKVKP--TLATYLSK-----NYSYVIHAKIKA 205

DQ 171 SPDGPEVGIKIDNEVIA---GPSECOCTCNQFPQVASEKSKVGNVTNCAYSCHSPALA 227

QY 206 VORS 209

DQ 228 ESHS 231

RESULT 11

JC7127

frizzled protein 4 - human

C:Species: Homo sapiens (man)

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001

C:Accession: JC7127

R:Kirikoshi, H.; Sagara, N.; Kolke, J.; Tanaka, K.; Sekihara, H.; Hirai, M.; Katoh, M.

Biochem. Biophys. Res. Commun. 264, 955-961, 1999

A:Title: Molecular cloning and characterization of human frizzled-4 on chromosome 11q14-

A:Reference number: JC7127; PMID:10544037

A:Accession: JC7127

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-537 <KIR>

A:Cross-references: GB:AB032417; DBJ:AB032417; NID:g6277265; PID:g6277266

C:Genetics:

A:Gene: FZD4

A:Map position: 11 region q14 - q21

C:Superfamily: fruit fly frizzled protein

Query Match

Best Local Similarity 14.1%; Score 265; DB 2; Length 537;

Matches 74; Conservative 47; Mismatches 107; Indels 30; Gaps 8;

QY 3 LSLTVALCLWLHLALGVGCA-----APCEAVRIPMCRHMPNITRMPNHLHSTQENAI 55

DQ 3 LSLTVALCLWLHLALGVGCA-----APCEAVRIPMCRHMPNITRMPNHLHSTQENAI 55

Db 17 VGLSLGLLLQLLLLLLGPARGFGDEERRRCDPTRISMCQNLGYNVTKMPLNLVGHLEQTDAE 76

QY 56 LAIEQYEEELVDVNCASVLRFFFCAMVAPICTLEFLHDPKCKSVQCORARDCEPLMKMY 115

Db 77 LQLTTTPTLIQYCCSSQLOFFLGSVVPMT-EXINIPGCGMGCLSVKRRCEPVLPKEP 135

QY 116 NISWPESLACDELPUYD--RGVCISPEAIVTDLPEDVKWIDITPDMVMQERPLDVKCKRL 173

Db 136 GFAPESLNCCKFPQNDHNMCMGPG-----DEEVPLPKPTIQPGEB-----CHSV 184

QY 174 SPDRCKCKVKPTLATYLSKNYSYVIHAKI-----KAVORSQGCNEVTVVDVKELPK 225

Db 185 GTNSDQYIWKSLNCLVKCGYDAGLYSRSAKEFTDLMVAVWASLC-FISTAPTVLTLFI 243

QY 226 SSSPIRTOVPLITNSSC 243

Db 244 DSRFSYPERPIFLSMC 261

RESULT 12

JC7312

frizzled-3 protein - human

C:Species: Homo sapiens (man)

C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 02-Mar-2001

C:Accession: JC7312

R:Sala, C.F.; Formenti, E.; Terstappen, G.C.; Caricasole, A.

Biochem. Biophys. Res. Commun. 273, 27-34, 2000

A:Title: Identification, gene structure, and expression of human frizzled-3 (FZD3).

A:Reference number: JC7312

A:Accession: JC7312

A:Molecule type: mRNA

A:Residues: 1-666 <SAL>

A:Cross-references: GB:AJ27242

A:Experimental source: brain

C:Comment: This protein, a seven-transmembrane receptor belonging to the frizzled fam

nositol levels in cells.

C:Genetics:

A:Gene: fzd3

A:Map position: 8p21

C:Superfamily: fruit fly frizzled protein

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 14.0%; Score 262.5; DB 2; Length 666;

Matches 61; Conservative 32; Mismatches 55; Indels 27; Gaps 8;

QY 7 VALCLW-LHLALGVGCA---PCEAVRIPMCRHMPNITRMPNHLHSTQENAILAIEQY 61

DQ 6 IVPSLWPLTVPMGHIGGHSLSFCEPITLRMCQDLPTNTTFMPLNLHRYDOOTAAALAMEPP 65

QY 62 EELVDVNCASVLRFFFCAMVAPICTLEFLHDPKCKSVQCORARDCEPLMKMYNISWPE 121

DQ 66 HPWNLDCSRDFPFICALYAPIC-MEYGRVTL-PCRRLCQRAYSCSKLMENFGVPWPE 123

QY 122 SLACDELPE---VYDRGVCT-----SPEAIVTD---LPEDYKWDITPDM 159

DQ 124 DMESCRFPDCEPYPRLDVNLNLAGETEGAPVAVQRDYGFWCPRLEK---IDPDL 175

RESULT 13

T31690

hypothetical protein F27E11.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Mar-2001

C:Accession: T31690

R:Wamsley, P.; Keppler, D.

submitted to the EMBL Data Library, July 1997

A:Description: The sequence of C. elegans cosmid F27E11.

A:Reference number: Z21069

A:Accession: T31690

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-605 <WAM>

A:Cross-references: EMBL:AF016413; PIDN:AA65257.1; GSPDB:GN00023; CBSP:F27E11.3
A:Experimental source: strain Bristol N2; clone F27E11

C:Genetics:

A:Gene: CESP:F27E11.3

A:Map position: 5

A:Introns: 28/3; 454/1; 520/1; 562/1

C:Superfamily: fruit fly frizzled protein

Query Match 12.1%; Score 226.5; DB 2; Length 605;
Best Local Similarity 29.5%; Pred. No. 1.6e-10;
Matches 59; Conservative 27; Mismatches 77; Indels 37; Gaps 7;

QY 39 ITRMNLHSHSTQENAILAEQYEEELVDVNCASVLRFFFCAMYPACTLEFLHDPKPKCK 98

Db 1 MTSFNSGHEKQEEAGLEVHQFYPLVEGCFQHLKFLCTWTPTICQ-ENYDKPILPCM 59

QY 99 SVCORARDCEPLMKMNYNSWPSLACDELP-----VYDRGVCISPEAIVTDLP----- 147

Db 60 ELCVEARSKCSPIMAKYGRFWPETUSCEALPKMSDOMSTGNICAAP----PDPKKQHKG 115

QY 148 -----EDVKWIDITPDMVQERPLVDCKRLSPDRCKKVKP--TLATYLSK- 193

Db 116 HHKKNQONQNHVSPDPEVGISKIDNEVIA---GFSECOCTCNPQFQVASEKSKV 172

QY 194 -----NYSYVIHAKIRAVORS 209

Db 173 GNVNTCAVSCSPALAESHS 192

RESULT 14

frizzled-6 protein precursor - human

C:Species: Homo sapiens (man)

C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 02-Mar-2001

C:Accession: JE0164

R:Tokuhara, M.; Hirai, M.; Atomi, Y.; Terada, M.; Katoh, M.

Biochem. Biophys. Res. Commun. 243, 622-627, 1998

A:Title: Molecular cloning of human frizzled-6.

A:Reference number: JE0164; MUID:98153814; PMID:9480858

A:Accession: JE0164

A:Molecule type: mRNA

A:Residues: 1-706 <TOR>

A:Cross-references: GB:AB012911; NID:g3062802; PIDN:BA25686.1; PID:g3062803

C:Comment: This protein is receptor for selected glycoproteins in development and carcin

C:Genetics:

A:Gene: Hfz6

A:Map position: 8q22.3-q23.1

C:Superfamily: fruit fly frizzled protein

C:Keywords: glycoprotein

F:1-18/Domain: signal sequence #status predicted <SIG>

F:201-222/Domain: transmembrane #status predicted <TM1>

F:233-255/Domain: transmembrane #status predicted <TM2>

F:281-312/Domain: transmembrane #status predicted <TM3>

F:324-345/Domain: transmembrane #status predicted <TM4>

F:370-393/Domain: transmembrane #status predicted <TM5>

F:417-436/Domain: transmembrane #status predicted <TM6>

F:473-495/Domain: transmembrane #status predicted <TM7>

F:38.352/Binding site: carbohydrate (Asn) #status predicted

Query Match 11.7%; Score 220; DB 2; Length 706;
Best Local Similarity 31.9%; Pred. No. 6.4e-10;
Matches 44; Conservative 27; Mismatches 63; Indels 4; Gaps 3;

QY 1 MFLSLVALCLHLALVGRGAPCEAVRIPMCRHMPWNIITRPNHLHSHSTQENAILAEQ 60

Db 3 MFTFLT--CIFPLLRGHSLTCTCPITVPRCKMKNWNTFFPNLMGHYDQSIAAVEMEH 60

QY 61 YEELDVNCSAVLRFFFCAMYPACTLEFLHDPKPKCKVQCORARDCCEPLMKMNYNSWP 120

Db 61 FLPLANLECSPIETFLCKAFVPTC-IEQIH-VVPCPKLCEKYSVSDCKKLIDTFTGIRWP 118

QY 121 ESLACDELPVYDRGVCIS 138

Job time : 23 secs

Db 119 EELECDRLQYCDETVPVT 136

RESULT 15

frizzled protein-2 - human

C:Species: Homo sapiens (man)

C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999

C:Accession: JE0174

R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.

Biochem. Biophys. Res. Commun. 247, 287-293, 1998

A:Title: Tissue restricted expression of two human frzbs in preadipocytes and pancrea

A:Reference number: JE0174; MUID:98308108; PMID:9642118

A:Accession: JE0174

A:Molecule type: mRNA

A:Residues: 1-295 <HUA>

C:Genetics:

A:Map position: 4q

Query Match 11.6%; Score 218; DB 2; Length 295;

Best Local Similarity 26.3%; Pred. No. 3.4e-10;

Matches 62; Conservative 41; Mismatches 91; Indels 42; Gaps 9;

QY 6 LVALCLMLHLALG-----VRGAPCEAVRIPMCRHMPWNI-----TRMPNHLHSH 49

Db 8 LLLFLASHCHCLGARGLEFLFGQPDFSYKRSNCKIPANLQCHGIEYQNMRLPNLLGHE 67

QY 50 TOENAILATEQYEEELVDVNCASVLRFFFCAMYPACTLEFLHDPKPKCKVQCORARDCCE 109

Db 68 TMKEVLEQAGAWIPLVWKQCHDPTKFLCLSLFAPVC-LOOLDETIQCHSLCQVQKDRCA 126

QY 110 PLMKMNYNSWPSLACDELPVYDRGVCISPEAIVTDLDPEDVKWIDITPDMVQERPLDVD 169

Db 127 PVMSAFGFPPDMLCEDRFP-QDNDLCIPLASSDHLLP-----ATEAPKVC 173

QY 170 -CKRLSPD-----RCKCK-----KVKPTLATYLSKNYSYVIHAKIKAVOR-SCNE 213

Db 174 ACKNKNDNDNDIMETLCKNDFALKIKVKETIYNRDTKIILETKSKTIYKLVGSE 229

Search completed: March 7, 2003, 11:25:27

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 7, 2003, 11:20:34 ; Search time 13 Seconds
(without alignments)
1103.908 Million cell updates/sec

Title: US-09-909-775-2

Perfect score: 1879

Sequence: 1 MFLSLVALCLWLHLALGVR.....SPKKNIKTRSAOKRTNPKRV 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	831	44.2	325	1 FRZB_BOVIN	Q95117 bos taurus
2	830	44.2	323	1 FRZB_MOUSE	P97401 mus musculus
3	828	44.1	325	1 FRZB_HUMAN	Q92765 homo sapien
4	338.5	18.0	585	1 F2D5_HUMAN	Q13467 homo sapien
5	331	17.6	577	1 F2D5_MOUSE	Q9eqd0 mus musculus
6	318	16.9	694	1 FR22_DROME	Q9vpx3 drosophila
7	312	16.6	591	1 F2D9_HUMAN	Q00144 homo sapien
8	310	16.5	592	1 F2D9_MOUSE	Q9r216 mus musculus
9	308.5	16.4	549	1 F2D7_XENLA	Q9pkx8 xenopus lae
10	308	16.4	694	1 F2D8_HUMAN	Q9h461 homo sapien
11	307.5	16.4	642	1 F2D1_MOUSE	Q70421 mus musculus
12	306	16.3	567	1 F2D7_CHICK	Q57329 gallus gall
13	306	16.3	581	1 F2D8_XENLA	Q93274 xenopus lae
14	305.5	16.3	592	1 F2D1_CHICK	Q57328 gallus gall
15	305	16.2	685	1 F2D8_MOUSE	Q61091 mus musculus
16	303	16.1	559	1 F2D1_XENLA	Q9i9m5 xenopus lae
17	301.5	16.0	559	1 F2D5_XENLA	P58421 xenopus lae
18	300.5	16.0	648	1 F2D1_HUMAN	Q9up38 homo sapien
19	299.5	15.9	574	1 F2D7_HUMAN	Q95084 homo sapien
20	299	15.9	583	1 FR12_DROVI	Q24760 drosophila
21	298.5	15.9	572	1 F2D7_MOUSE	Q61090 mus musculus
22	294	15.6	641	1 F2D1_RAT	Q08463 rattus norv
23	293.5	15.6	551	1 F2D2_XENLA	Q9puu6 xenopus lae
24	293.5	15.6	580	1 F2D8_XENLA	Q9w742 xenopus lae
25	293	15.6	565	1 F2D2_HUMAN	Q14332 homo sapien
26	293	15.6	570	1 F2D2_MOUSE	Q9jip6 mus musculus
27	293	15.6	570	1 F2D2_RAT	Q08464 rattus norv
28	292	15.5	585	1 F210_CHICK	Q9pwh2 gallus gall
29	289	15.4	581	1 FR12_DROME	P18537 drosophila
30	287.5	15.3	523	1 F2D2_CHICK	Q9ia06 gallus gall
31	285.5	15.2	586	1 F2D4_XENLA	Q9deb5 xenopus lae
32	282	15.0	581	1 F210_HUMAN	Q9ulw2 homo sapien
33	271.5	14.4	523	1 F2D4_XENLA	Q9pt62 xenopus lae

ALIGNMENTS

RESULT 1

ID	FRZB_BOVIN	STANDARD;	PRT;	325 AA.
AC	Q95117;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Frizzled-related protein precursor (Frzb-1).			
GN	FRZB OR FRZB1.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cartilage;			
RX	MEDLINE=96421609; PubMed=8824257;			
RA	Hoang B., Moos M. Jr., Vukicevic S., Luyten F.P.;			
RT	"Primary structure and tissue distribution of FRZB, a novel protein related to Drosophila frizzled, suggest a role in skeletal morphogenesis."			
RT	J. Biol. Chem. 271:26131-26137(1996).			
RN	[2]			
RP	INTERACTION BETWEEN THE FZ DOMAIN AND WNT PROTEINS.			
RX	MEDLINE=97470942; PubMed=9326585;			
RA	Lin K., Wang S., Julius M.A., Kitajewski J., Moos M. Jr., Luyten F.P.;			
RT	"The cysteine-rich frizzled domain of Frzb-1 is required and sufficient for modulation of Wnt signaling."			
RT	Proc. Natl. Acad. Sci. U.S.A. 94:11196-11200(1997).			
CC	-!- FUNCTION: MAY BE INVOLVED IN MORPHOGENESIS OF SKELETON. MAY ALSO ACT AS A SOLUBLE WNT-BINDING PROTEIN THAT MAY ANTAGONIZE WNT SIGNALING.			
CC	-!- SUBCELLULAR LOCATION: Secreted (Probable).			
CC	-!- DOMAIN: The FZ domain is involved in binding with Wnt ligands.			
CC	-!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.			
CC	-!- SIMILARITY: CONTAINS 1 NTR DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL: U24164; AAC48652.1; ..			
DR	InterPro: IPR000024; Fz_domain.			
DR	InterPro: IPR001134; Netrin_C.			
DR	Pfam: PF01392; FZ; 1.			
DR	Pfam: PF01759; NTR; 1.			
DR	SMART: SM00063; FRL; 1.			
DR	PROSITE: PS50038; FZ; 1.			
KW	Glycoprotein; Signal.			
FT	SIGNAL 1 32			POTENTIAL.
FT	CHAIN 33 325			FRIZZLED-RELATED PROTEIN.

34	265	14.1	537	1 FZD4_HUMAN	Q9ulv1 homo sapien
35	263.5	14.0	666	1 FZD3_MOUSE	Q61086 mus musculus
36	262.5	14.0	664	1 FZD3_XENLA	Q42579 xenopus lae
37	262.5	14.0	666	1 FZD3_HUMAN	Q9npq1 homo sapien
38	260	13.8	525	1 FZD4_CHICK	Q9ia05 gallus gall
39	259	13.8	538	1 FZD4_RAT	Q9qzh0 rattus norv
40	255	13.6	537	1 FZD4_MOUSE	Q61088 mus musculus
41	228	12.1	705	1 FR24_DROME	Q9nbw1 drosophila
42	220	11.7	706	1 FZD6_HUMAN	O60353 homo sapien
43	215.5	11.5	709	1 FZD6_MOUSE	Q61089 mus musculus
44	215	11.4	1042	1 COR1_HUMAN	Q9y5q5 homo sapien
45	204	10.9	1113	1 COR1_MOUSE	Q92319 mus musculus

```
FT DOMAIN 33 150 FZ.
FT SITE 165 294 NTR.
FT CARBOHYD 49 49 SER-RICH.
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 325 AA; 36234 MW; 39E337A9C5E98B63 CRC64;

Query Match 44.2%; Score 831; DB 1; Length 325;
Best Local Similarity 51.4%; Pred. No. 3.1e-62;
Matches 166; Conservative 48; Mismatches 77; Indels 32; Gaps 8;

QY 3 LSIIVLCLMLHLALGVGAPCEAVRIPMCRHMPWNTTRPNHLHSHSTQNAIILAIOYE 62
DB 16 LLVLAALCL-LRVP-GAARAAACEPVRIPLCKSLPWNMTKPNHLHSHSTQNAIILAIOQE 73
QY 63 ELVDVNCISAVLRFFECAMYPICITLFLHDPKPKSVCCORARDCEPLKMKMYHNSWPES 122
DB 74 GLLGTHCSPLLFLCLMAYAPICITDQHEPIKPKSVCCAROCCEPILIKYHNSWPES 133
QY 123 LACDELVPYDRGVCISPEAIVT-----DLPEVKWIDITPDMMVQERPLDVKRLSPDRC 178
DB 134 LACDELVPYDRGVCISPEAIVTADGAPMDSS-----NGNCRGASSERC 178
QY 179 KCKVKETLATYLSKNYSYVIHAKIKAVQSGCNEVTVYDVKEIFKSS-SPIPTQVPL 237
DB 179 KCKPVRAVATQRTYFNRYNYIRAKVKEI-KTKCHDVTAVVEKILKASLVNIPRETVNL 237
QY 238 ITNSSCCPHLPDHLINCY--EWSRMMLLENCLVEKWRDOLSKRSIOWEERLEOR 295
DB 238 YTSGLCPPLNNEEVLINGYEDEERSRLLVEGSAERKWKDLGKVRWDMKLRHLG 297
QY 296 RTVOD-----KKKTAGRTSRS 311
DB 298 LNTSSSHSDSTQSKPGRNSNS 320

RESULT 2
FRZB_MOUSE STANDARD; PRT; 323 AA.
ID FRZB_MOUSE
AC P97401; O09075; O09093;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DE Frizzled-related protein precursor (Frzb-1) (Frezzed) (Fritz)
DE (Secreted frizzled-related sequence protein 3) (sFRP-3).
GN FRZB OR FRZB1 OR FRE OR SFRP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236495; PubMed=9118218;
RA Leyns L., Bouwmeester T., Kim S.H., Piccolo S., De Robertis E.M.;
RT "Frzb-1 is a secreted antagonist of Wnt signaling expressed in the
RT Spemann organizer."
RL Cell 88:747-756(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97250455; PubMed=9096311;
RA Rattnner A., Hsieh J.C., Smallwood P.M., Gilbert D.J., Copeland N.G.,
RA Jenkins N.A., Nathans J.;
RT "A family of secreted proteins contains homology to the cysteine-rich
RT ligand-binding domain of frizzled receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 94:2859-2863(1997).
RN [4]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Tamaoka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weiss C., Whittaker C., Wilming L.,
RA Wyshaw-Borls A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
CC -1- FUNCTION: MAY BE INVOLVED IN MORPHOGENESIS OF SKELETON. MAY ALSO
CC ACT AS A SOLUBLE WNT-BINDING PROTEIN THAT MAY ANTAGONIZE WNT
CC SIGNALING.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- DOMAIN: The Fz domain is involved in binding with Wnt ligands (By
CC similarity).
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 NTR DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U68058; AAC53135.1; -
CC EMBL: U61905; AAB51300.1; -
CC EMBL: U88568; AAC53147.1; -
CC EMBL: AK019093; BAB31542.1; -
CC MGD: MGI:892032; Frzb.
CC InterPro: IPR000024; Fz_Domain.
CC InterPro: IPR001134; Netrin_C.
CC Pfam: PF01392; Fz; 1.
CC SMART: SM00063; FRI; 1.
CC PROSITE: PS50038; FZ; 1.
CC Glycoprotein: Signal.
KW SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 323 FRIZZLED-RELATED PROTEIN.
FT DOMAIN 33 150 FZ.
FT DOMAIN 165 294 NTR.
FT SITE 301 318 SER/THR-RICH.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 323 AA; 36011 MW; 3F1456F8CF97740 CRC64;

Query Match 44.2%; Score 830; DB 1; Length 323;
Best Local Similarity 50.8%; Pred. No. 3.7e-62;
Matches 166; Conservative 50; Mismatches 77; Indels 34; Gaps 9;

QY 3 LSIIVLCLMLHLALGVGAPCEAVRIPMCRHMPWNTTRPNHLHSHSTQNAIILAIOYE 62
DB 16 LLVLAALCL-LQVP-GAARAAACEPVRIPLCKSLPWNMTKPNHLHSHSTQNAIILAIOQE 73
QY 63 ELVDVNCISAVLRFFECAMYPICITLFLHDPKPKSVCCORARDCEPLKMKMYHNSWPES 122
DB 74 GLLGTHCSPLLFLCLMAYAPICITDQHEPIKPKSVCCAROCCEPILIKYHNSWPES 133
QY 123 LACDELVPYDRGVCISPEAIVT-----DLPEVKWIDITPDMMVQERPLDVKRLSPDRC 178
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|||||
Db 134 LACDELVDYDGVGVCISPEAIVTAGDGFPMDS-----TCHCRGASSERC 178
QY 179 KCKVPTATLTKYVVIHAKIKAVORSGNEVTTVVDVKEIFKSS-SPIPTQVPL 237
Db 179 KCPVATOKTYFRNNYVIRAKVEKMK-CHDTAVVEVEIKLAKLVNIPRTVNL 237
QY 238 ITNSSCQCCHILPHODVLINCY--EWRSRMMLLENCLVEKWRDOLSKRSIOWEERLO--- 292
Db 238 YTTSGCLCPPLTVEEVINGYEDEERSRLLVGEGSIAEKWKDRGLCKVKRWDMKLRHLG 297
QY 293 -----EQRTVDDKKTKAGTNRSPPK 315
Db 298 LGKTDASDSTONOK--SGRNSNPPAR 322

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RESULT 3

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FRZB_HUMAN STANDARD; PRT; 325 AA.
ID FRZB_HUMAN Q92765; O00181; Q99686;
AC Q92765; O00181; Q99686;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled-related protein precursor (Frzb-1) (Frizzled) (Fritz).
GN FRZB OR FRZB1 OR PRE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96421609; PubMed=8824257;
RA Hoang B., Moos M. Jr., Yukićević S., Luyten F.P.;
RT "Primary structure and tissue distribution of FRZB, a novel protein related to Drosophila frizzled, suggest a role in skeletal morphogenesis."
RL J. Biol. Chem. 271:26131-26137(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Mayr T., Deutsch U., Kuehl M., Drexler H.C.A., Lottspeich F.,
RA Deutmann R., Wedlich D., Risau W.;
RT "Fritz: a secreted frizzled-related protein that inhibits Wnt activity."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97236495; PubMed=9118218;
RA Leyns L., Boumeester T., Kim S.-H., Piccolo S., de Robertis E.M.;
RT "Frzb-1 is a secreted antagonist of Wnt signaling expressed in the Spemann organizer."
RL Cell 88:747-756(1997).
CC -|- FUNCTION: MAY BE INVOLVED IN MORPHOGENESIS OF SKELETON. MAY ALSO ACT AS A SOLUBLE WNT-BINDING PROTEIN THAT MAY ANTAGONIZE WNT SIGNALING.
CC -|- SUBCELLULAR LOCATION: Secreted (Probable).
CC -|- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CARPILAGENOUS CORES OF THE LONG BONE DURING EMBRYONIC AND FETAL DEVELOPMENT AND IN THE APPENDICULAR SKELETON (6-13 WEEKS). AT 13 WEEKS OF GESTATION, TRANSCRIPTS WERE PRESENT IN EARLY CHONDROBLASTS OF THE TARSAL BONES OF THE FOOT, THE CARPAL BONES OF THE HANDS AND THE EPIPHYSIS OF LONG BONES. HIGHLY EXPRESSED IN PLACENTA AND HEART. FOLLOWED BY BRAIN, SKELETAL MUSCLE, KIDNEY AND PANCREAS. WEAKLY EXPRESSED IN LUNG AND LIVER.
CC -|- DOMAIN: The Fz domain is involved in binding with Wnt ligands (By similarity).
CC -|- SIMILARITY: CONTAINS 1 FRIZZLED (Fz) DOMAIN.
CC -|- SIMILARITY: CONTAINS 1 NTR DOMAIN.

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CC -----
CC EMBL: 024163; AAC50736.1; -
DR EMBL: 091903; AAB51298.1; -
DR EMBL: 068057; AAC51217.1; -
DR Genew: HGNC:3959; FRZB.
DR MIM: 605083; -
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR001134; Netrin_C.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF01759; NTR; 1.
DR SMART: SM00063; FRI; 1.
DR PROSITE: PS50038; FZ; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 32
FT CHAIN 33 325
FT DOMAIN 33 150
FT DOMAIN 165 294
FT SITE 301 318
FT CARBOHYD 49 49
FT CONFLICT 63 63
FT CONFLICT 106 106
FT CONFLICT K -> N (IN REF. 1).
SQ SEQUENCE 325 AA; 36254 MW; 8337C51BBA9A4B07 CRC64;

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Query Match 44.1%; Score 828; DB 1; Length 325;
Best Local Similarity 50.8%; Pred. No. 5.4e-62;
Matches 164; Conservative 51; Mismatches 78; Indels 30; Gaps 8;
QY 3 LSLVALCLMLHLALGVGAPCAVRIPMCRHMPWNTTRMPNHLHSTOENALIAEIOYE 62
Db 16 LLALALCL-LRVP-GARAAACEPVRIPLCKSLPWNTRMPNHLHSTOENALIAEIOFE 73
QY 63 ELVDVNCASVAVRFFFCAMYPACTLEFLHDPIPKCSVCORARDCEPLMKMYNHSWPE 122
Db 74 GLUGTHCSPLDLFLCALMYPACTIDFQHEPIPKCSVCERAROGCEPILIKYRHSWPN 133
QY 123 LACDELVDYDGVGVCISPEAIVT-----DLPEVKWIDITPMVQERPLDVKRLSPDRC 178
Db 134 LACEELVDYDGVGVCISPEAIVTAGDGFPMDS-----NGNCRGASSERC 178
QY 179 KCKVPTATLTKYVVIHAKIKAVORSGNEVTTVVDVKEIFKSS-SPIPTQVPL 237
Db 179 KCPVATOKTYFRNNYVIRAKVEI-KTKCHDTAVVEVEIKLAKLVNIPRTVNL 237
QY 238 ITNSSCQCCHILPHODVLINCY--EWRSRMMLLENCLVEKWRDOLSKRSIOWEERLOEOR 295
Db 238 YTTSGCLCPPLNVEEVIINGYEDEERSRLLVGEGSIAEKWKDRGLCKVKRWDMKLRHLG 297
QY 296 RTVQDKKKTKAGTNR-----SNP 313
Db 298 LSKSDSSNSDSTOSQKSGRNSNP 320

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RESULT 4

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FRZ5_HUMAN STANDARD; PRT; 585 AA.
ID FRZ5_HUMAN Q13467;
AC Q13467;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled 5 precursor (Frizzled-5) (Fz-5) (FzE5).
GN FZD5 OR HFZ5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=96224032; PubMed=8626800;

```


SEQUENCE OF 207-296 FROM N.A.
SPRAIN-C57BL/6; TISSUE=Prostate;
Johnson M.A., Greenberg N.M.;
Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
[3]
TISSUE SPECIFICITY
MEDLINE=96224032; PubMed=8626800;
Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P.,
Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;
*A large family of putative transmembrane receptors homologous to the
product of the *Drosophila* tissue polarity gene *frizzled*.;
J. Biol. Chem. 271:4468-4476(1996).
-1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
are coupled to the beta-catenin canonical signaling pathway, which
leads to the activation of dishevelled proteins, inhibition of
GSK-3 kinase, nuclear accumulation of beta-catenin and activation
of Wnt target genes. A second signaling pathway involving PKC and
calcium fluxes has been seen for some family members, but it is
not yet clear if it represents a distinct pathway or if it can be
integrated in the canonical pathway, as PKC seems to be required
for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
to involve interactions with G-proteins. May be involved in
transduction and intercellular transmission of polarity
information during tissue morphogenesis and/or in differentiated
tissues. Plays a role in yolk sac angiogenesis and in placental
vascularization. Binds to Wnt2, Wnt10B, Wnt5A, but not to Wnt2B or
Wnt4.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: Expressed in eye, kidney, lung, chondrocytes,
epithelial cells of the small intestine and goblet cells of the
colon.
-1- DEVELOPMENTAL STAGE: Expressed in the yolk sac, placenta, eye and
lung bud at 9.5 days post coitum (dpc). At 10.5 dpc, also
expressed in the placental blood vessel of embryonic origin.
-1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
similarity).
-1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
RECEPTORS.
-1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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EMBL; AF272146; AAC39355.1; -
EMBL; AF005203; AAC01953.1; -
MGD; MGI:108571; Fzd5.
InterPro: IPR000539; Frizzled.
InterPro: IPR000024; Fz_domain.
InterPro: IPR000832; GPCR_secretin.
Pfam; PF01392; Fz; 1.
Pfam; PF01534; Frizzled; 2.
PRINTS; PR00489; FRIZZLED.
SMART; SM00063; FRI; 1.
PROSITE; PS50038; FZ; 1.
PROSITE; PS50261; G-PROTEIN_RECPT_F2_4; 1.
Multigene family; G-protein coupled receptor; Transmembrane;
Developmental protein; Glycoprotein; Signal.
SIGNAL 1 26
POTENTIAL
FT CHAIN 27 577 FRIZZLED 5.
FT DOMAIN 27 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 255 1 (POTENTIAL).
FT DOMAIN 256 267 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 267 287 2 (POTENTIAL).
FT DOMAIN 288 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 332 3 (POTENTIAL).
FT DOMAIN 333 354 4 (POTENTIAL).
FT TRANSMEM 355 375 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 376 398 EXTRACELLULAR (POTENTIAL).

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ihegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirski R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasatman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
CC are coupled to the beta-catenin canonical signaling pathway, which
CC leads to the activation of dishevelled proteins, inhibition of
CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
CC of Wnt target genes. A second signaling pathway involving PKC and
CC calcium fluxes has been seen for some family members, but it is
CC not yet clear if it represents a distinct pathway or if it can be
CC integrated in the canonical pathway, as PKC seems to be required
CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
CC to involve interactions with G-proteins. Required to coordinate
CC the cytoskeletons of epidermal cells to produce a parallel array
CC of cuticular hairs and bristles.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- DEVELOPMENTAL STAGE: Expression starts at stage 6 in all cells
CC between 15 and 70 per cent of egg length, including the
CC invaginating cells of the ventral furrow. Stripe pattern is
CC emerging by early stage 8. From stage 9 and continuing throughout
CC embryogenesis, expression is seen in the developing CNS. At stage
CC 10, expressed in 15 stripes in the presumptive head and trunk
CC regions, in the posterior midgut primordium, in a subset of cells
CC of anterior midgut invagination and in the procephalic lobe. At
CC stage 12, expression declines in epidermis and increases in the
CC midgut and visceral mesoderm. At stage 17, only expressed in the
CC CNS, hindgut and dorsal vessel.
CC -1- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of
CC the Wnt/beta-catenin signaling pathway (By similarity).
CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands.
CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
CC RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
CC -----
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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL: U65589; AAC47273.1; -;
DR EMBL: AE003318; AAF49184.1; -;
DR FlyBase: FBgn0016797; Fz2.
DR InterPro: IPR000539; Frizzled.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR000832; GPCR_secretin.
DR Pfam: PF01534; Frizzled; 1.
DR Pfam: PF01392; Fz; 1.
DR PRINTS: PR00489; FRIZZLED.
DR SMART: SM00063; FRI; 1.
DR PROSITE: PS50038; FRI; 1.
DR PROSITE: PS50261; G_PROTEIN_RECEPT_F2_4; 1.
KW Multigene family; Receptor; G-protein coupled receptor; Transmembrane;
KW Developmental protein; Glycoprotein; Signal.

FT SIGNAL 1 22
FT CHAIN 23 694
FT DOMAIN 23 315
FT TRANSMEM 316 336
FT TRANSMEM 337 352
FT TRANSMEM 353 373
FT TRANSMEM 374 397
FT TRANSMEM 398 418
FT TRANSMEM 419 439
FT TRANSMEM 440 460
FT TRANSMEM 461 482
FT TRANSMEM 483 503
FT TRANSMEM 504 534
FT TRANSMEM 535 555
FT TRANSMEM 556 584
FT TRANSMEM 585 605
FT TRANSMEM 606 694
FT TRANSMEM 606 694
FT TRANSMEM 187 225
FT TRANSMEM 59 180
FT SITE 608 613
FT SITE 692 694
FT CARBOHYD 78 78
FT CARBOHYD 288 288
FT CONFLICT 55 55
FT CONFLICT 417 417
SQ SEQUENCE 694 AA; 75451 MW; 6C510F13CBFAFB096 CRC64;
Query Match 16.9%; Score 318; DB 1; Length 694;
Best Local Similarity 39.4%; Pred. No. 5.4e-19;
Matches 56; Conservative 25; Mismatches 37; Indels 24; Gaps 2;
QY 24 CEAVRIPMRHPWNIITRMPNHLHSHQENAILAIEQYELVDVNCNSAVLRFFFCAMYAP 83
DB 64 CEETIPMCRGICYNMTSPFNEMHETQDEAGLEWFLVEIKCSPDLKFLCSNYTP 123
QY 84 ICTLEFLHDPKCKSVQCRARDCEPLMKMYNHSWPSLACDELPPYDRGVGVCISPAIV 143
DB 124 IC-LDYHKPLPVCRSVCRARSCAPIMQOYSPFENPERMACEHLPLHG----- 171
QY 144 TDLPEDVKWIDITPDMNVQERP 165
DB 172 -----DPDNLCMEQP 181
RESULT 7
FZD9_HUMAN STANDARD; PRT; 591 AA.
ID FZD9_HUMAN
AC Q00144;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Frizzled 9 precursor (Frizzled-9) (Fz-9) (hFz9) (FzB6).
GN FZD9 OR FZD9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=9727293; PubMed=9147651;
RA Wang Y.-K., Samos H.C., Peoples R., Perez-Jurado L.A., Nusse R.,
RA Francke U.;
RT "A novel human homologue of the *Drosophila* frizzled wnt receptor gene
RT binds wingless protein and is in the Williams syndrome deletion at
RT 7q11.23.";
RL Hum. Mol. Genet. 6:465-472(1997).
RN [2]
RP SEQUENCE OF 269-329 FROM N.A.
RC TISSUE=Oesophageal carcinoma.
RX MEDLINE=98374323; PubMed=9707618;
RA Tanaka S., Akiyoshi T., Morl M., Wands J.R., Sugimachi K.;
RT "A novel frizzled gene identified in human esophageal carcinoma

SQ SEQUENCE 591 AA; 64466 MW; OD3784A78D0F0B2E5 CRC64;
 Query Match 16.6%; Score 312; DB 1; Length 591;
 Best Local Similarity 40.4%; Pred. No. 1.4e-18;
 Matches 63; Conservative 27; Mismatches 46; Indels 20; Gaps
 QY 8 ALCWLHLALG-----VRG----ACCEAVRIPMCRHMPWNITRPMNHLHHSTQEN 53
 ||||| | || ||||| ||||| : ||||| | : ||:
 Db 9 ALLWQLLAAGGALETGRFDPERGRAAPCAOAEVPEIMPCRGIGYNLTRPMLLGHSTSGE 68
 ||||| | || ||||| ||||| : ||||| | : ||:
 QY 54 AILAEIOVEELVDNVCSAVLRFFECAMYPICLTFLHPDPKCKSVQCORARDDCPLMK 113
 ||||| | || ||||| ||||| : ||||| | : ||:
 Db 69 AAABEAFAFLVQGVCHSHLRFLLCSUYAPMCT-DQVSTPIACRPMCBOARLRCAPIME 127
 : ||||| | || ||||| ||||| : ||||| | : ||:
 QY 114 MYNSWPESLACDELPPYDRGVGISPEAIYTDLPED 149
 : ||||| | || ||||| ||||| : ||||| | : ||:
 Db 128 QFNFGWPSLDLCARLPTRN-----DPHALCMEAPEN 158
 : ||||| | || ||||| ||||| : ||||| | : ||:
 RESULT 8
 FZD9 MOUSE STANDARD; PRT; 592 AA.
 ID FZD9_MOUSE AC Q9R216; O9CX16; O35494; O9R2B3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Frizzled-9 precursor (Frizzled-9) (Fz-9) (mfz9) (mfz3).
 FN FZD9 OR FZD3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomii;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
 RC STRAIN=129/SVJ; TISSUE=Brain;
 RX MEDLINE=99216417; PubMed=10198163;
 RA Wang Y.-K., Spoerle K., Paperna T., Schughart K., Francke U.;
 RT "Characterization and expression pattern of the frizzled gene Fzd9,
 RT the mouse homolog of FZD9 which is deleted in Williams-Beuren
 RT syndrome.";
 RL Genomics 57:235-248(1999).
 RN [2]
 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryonic head;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.;
 ET "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 SEQUENCE OF 44-592 FROM N.A.
 RA Van Raay T.J., Rasmussen J.T., Rao M.S.;
 RT "A novel mouse frizzled gene expressed in early neural development."
 RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 SEQUENCE OF 144-592 FROM N.A.
 RC STRAIN=BALB/c;

RA Calo L., Mimmack M.L., Keverne E.B., Emson P.C.;
 RT "Localization of the mouse frizzled gene mFzd3 in the olfactory
 RL epithelium and in the vomeronasal organ.";
 CC Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
 CC are coupled to the beta-catenin canonical signaling pathway, which
 CC leads to the activation of dishevelled proteins, inhibition of
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation
 CC of Wnt target genes. A second signaling pathway involving PKC and
 CC calcium fluxes has been seen for some family members, but it is
 CC not yet clear if it represents a distinct pathway or if it can be
 CC integrated in the canonical pathway, as PKC seems to be required
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
 CC to involve interactions with G-proteins. May be involved in
 CC transduction and intercellular transmission of polarity
 CC information during tissue morphogenesis and/or in differentiated
 CC tissues.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Localizes in the
 CC plasma membrane.
 CC -!- TISSUE SPECIFICITY: In the embryo, found in the neural tube, trunk
 CC skeletal muscle precursors (myotomes), limb skeletal anlagen,
 CC craniofacial regions and nephric ducts. In the adult, expression
 CC is abundant in heart, brain, testis and skeletal muscle. In the
 CC testis, expressed in all spermatogenic cell types. Lower levels in
 CC adult lung, liver and kidney. Barely detectable in spleen.
 CC Expressed also in chondrocytes.
 CC -!- DEVELOPMENTAL STAGE: Not detected at embryonic day 7 (E7), weakly
 CC at E11 and strongly at E15 and E17. Expression covers the entire
 CC neural tube at day 9.5 post-cultum (dpc), decreases at 10.5 dpc
 CC and becomes detectable only in the lumbar to tail regions at 11.5
 CC dpc. In the somites, expression begins at 10.5 dpc to become
 CC upregulated all along the rostrocaudal trunk axis at 11.5 dpc. In
 CC craniofacial territories, expression is first detected at 11.5 dpc
 CC in restricted areas of the nose, the maxillary mandibular and
 CC second branchial arch anlagen. At 11.5 dpc, predominantly
 CC expressed in restricted areas of the nose, dorsally to the eye and
 CC in the caudal pharyngeal region.
 CC -!- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of
 CC the Wnt/beta-catenin signaling pathway (By similarity).
 CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (Fz) DOMAIN.
 CC -!- CAUTION: Has been first described as Fzd3 in litterature.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: AF088850; AAD27789.1; -;
 CC EMBL: AK021164; BAB32311.1; -;
 CC EMBL: AF033585; AAB87503.2; -;
 CC EMBL: Y17709; CAB44237.1; -;
 CC MGD: MGI:1313278; Fzd9.
 CC InterPro: IPR000539; Frizzled.
 CC InterPro: IPR000024; Fz_domain.
 CC InterPro: IPR000832; GPCR_secretin.
 CC Pfam: PF01392; Fz; 2.
 CC PRINTS: PR00489; *FRIZZLED.
 CC SMART: SM00063; Fz1; 1.
 CC PROSITE: PS50038; Fz; 1.
 CC PROSITE: PS50261; G_PROTEIN_RECEP_F2_4; 1.
 CC KW Multigene family; G-protein coupled receptor; Transmembrane;
 CC Developmental protein; Glycoprotein; Signal.
 CC SIGNAL 1 23 POTENTIAL.
 CC FT CHAIN 24 522 FRIZZLED 9.
 CC DOMAIN 24 230 EXTRACELLULAR.

FT TRANSMEM 231 251 1 (POTENTIAL).
 FT DOMAIN 252 267 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 268 288 2 (POTENTIAL).
 FT DOMAIN 289 316 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 317 337 3 (POTENTIAL).
 FT DOMAIN 338 356 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 357 377 4 (POTENTIAL).
 FT DOMAIN 378 401 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 402 422 5 (POTENTIAL).
 FT DOMAIN 423 448 6 (POTENTIAL).
 FT TRANSMEM 449 469 7 (POTENTIAL).
 FT DOMAIN 470 509 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 510 530 7 (POTENTIAL).
 FT DOMAIN 531 552 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 553 574 FZ.
 FT SITE 575 594 LYS-THR-X-X-TRP MOTIF.
 FT CARBOHYD 595 614 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 615 634 S -> P (IN REF. 3).
 FT CONFLICT 635 654 QL -> HC (IN REF. 2).
 FT CONFLICT 655 674 L -> F (IN REF. 2).
 FT CONFLICT 675 694 P -> S (IN REF. 4).
 FT CONFLICT 695 714 E -> K (IN REF. 4).
 FT CONFLICT 715 734 A -> P (IN REF. 3).
 FT CONFLICT 735 754 G -> D (IN REF. 3).
 FT CONFLICT 755 774 V -> F (IN REF. 4).
 FT CONFLICT 775 794 L -> P (IN REF. 2).
 SQ SEQUENCE 592 AA; 64994 MW; 21B2D4F8C5232965 CRC64;
 Query Match 16.5%; Score 310; DB 1; Length 592;
 Best Local Similarity 39.7%; Pred. No. 2,1e-18;
 Matches 62; Conservative 28; Mismatches 46; Indels 20; Gaps* 4;
 QY 8 ALCLWLHLALG-----VRG---APCEAVRIPMGRHMPNITRPNHLHSTOEN 53
 DB 10 ALLWOLLATGGALEIGRDPGRGPACQAMEIPMCRGICYNITRPNLLGHTSQGE 69
 QY 54 AILAIQYEEELVDVNCASVLRFFCFYAPICFLEFLHDPKPKSVQCORARDDCEPLMK 113
 DB 70 AAQAQAEFSLVOYGCHSLRFLCSLYAPMCT-DQVSTPIPACRPMCEQARLCAPIME 128
 QY 114 MYNHSWPESLACDELVPYDRGVCISPEAIVTDLPED 149
 DB 129 QNFNGWPSLDLCARLPTRN-----DPHALCMEAPEN 159
 RESULT 9
 FZD7_XENLA STANDARD; PRT; 549 AA.
 AC Q9PUK8; Q9W743; Q9W703; Q9PMN7; Q9TIB3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 7 precursor (Frizzled-7) (Fz-7) (Xiz7).
 GN FZ7.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_Taxid=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99376692; PubMed=10446283;
 RA Wheeler G.N., Hoppler S.;
 RT "Two novel Xenopus frizzled genes expressed in developing heart and
 RL brain.";
 RL Mech. Dev. 86:203-207(1999).
 RN [2]
 RP SEQUENCE FROM N.A., COUPLING TO BETA-CATENIN PATHWAY, AND PKC
 RP ACTIVATION.
 RC TISSUE=Neurula;
 RC MEDLINE=20193498; PubMed=10727861;
 RA Medina A., Reintsch W., Steinbeisser H.;

FT SITE	620	625	LYS-THR-X-X-X-TRP MOTIF.
SITE	640	642	PDZ-BINDING.
CARBOHYD	125	125	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	226	226	N-LINKED (GLCNAC. . .) (POTENTIAL).
CONFLICT	341	341	P -> R (IN REF. 2).
CONFLICT	352	352	S -> F (IN REF. 2).
SEQUENCE	642 AA:	70955 MW:	0AAD0C0DC820B6CE CRC64;
Query Match	16.4%;	Score 307.5;	DB 1; Length 642;
Best Local Similarity	37.6%;	Pred. No. 3.7e-18;	
Matches	64;	Conservative	24; Mismatches 39; Indels 43; Gaps 5;
QY	9 LCLWL---	HLALGVRG-	-----AP-----CEAVR 28
Ddb	56 LLLLEALL	LLLVRAQAAGVSGPQQAPPPPPQPGSQQYNGRGISIPDHGYCOPIS 115	: : :
QY	29 IPMCRHMPNITR	PMNHLHSHSTQENAILAIEQYEEELVDVNCYSAVLRFFFCAYAPICTLE 88	: : : : : : : :
Ddb	116 IPLCTDMAYNOT	IMPMLNLLGHTNQEDAGLEVHQYPLVKVQCSAELKFFCLSMYAPVCTV- 174	: : : : : : : :
QY	89 FLUHPDKPKSCY	CCORARDCEPLMKMYNHSWPESLACDELPVYDRG-VCI 137	: : : : : : :
Ddb	175 -LEQALPPCRSL	CERAROCCEALMKNKFGQWDTLCKEKFVPHGAGELCV 223	: : : : : :
RESULT 12	FEZD7_CHICK		
IID	FZD7_CHICK	STANDARD;	PRT: 567 AA.
AC	O57329; Q91A04;		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Frizzled 7 precursor (Frizzled-7) (Fz-7) (CFz-7).		
GN	FZD7 OR FZ7.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RRN	[1]		
RRP	SEQUENCE FROM N.A.		
RRP	TISSUE=Limb bud;		
RRC	MEDLINE=98260739; PubMed=95598377;		
RRR	Kengaku M., Twombly V., Tabin C.;		
RRR	"Expression of Wnt and Frizzled genes during chick limb bud		
RRT	development.";		
RRT	Cold Spring Harb. Symp. Quant. Biol. 62:421-429(1997).		
RRR	[2]		
RRN	SEQUENCE FROM N.A.		
RRP	TISSUE=Embryo;		
RRC	MEDLINE=20245319; PubMed=10781956;		
RRR	Stark M.R., Biggs J.J., Schoenwolf G.C., Rao M.S.;		
RRR	"Characterization of avian frizzled genes in cranial placode		
RRT	development.";		
RRT	Mech. Dev. 93:195-200(2000).		
CCC	-!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors		
CCC	are coupled to the beta-catenin canonical signaling pathway, which		
CCC	leads to the activation of dishevelled proteins, inhibition of		
CCC	GSK-3 kinase, nuclear accumulation of beta-catenin and activation		
CCC	of Wnt target genes. A second signaling pathway involving PKC and		
CCC	calcium fluxes has been seen for some family members, but it is		
CCC	not yet clear if it represents a distinct pathway or if it can be		
CCC	integrated in the canonical pathway, as PKC seems to be required		
CCC	for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem		
CCC	to involve interactions with G-proteins. May be involved in		
CCC	transduction and intercellular transmission of polarity		
CCC	information during tissue morphogenesis and/or in differentiated		
CCC	tissues.		
CCC	-!- SUBCELLULAR LOCATION: Integral membrane protein.		
CCC	-!- TISSUE SPECIFICITY: Expressed broadly in cranial ectoderm. Also		
CCC	expressed in the developing somites and in other cranial placodes,		
CCC	including the olfactory, lens, otic placodes (lateral half of the		
CCC	vesicle) and epibranchial placodes. Low level of expression in all		

the mesoderm derivatives in the limb buds.

-1- DEVELOPMENTAL STAGE: First detected as stage 6 in the forming neural tube and somites, but not in trunk surface ectoderm. By stage 8, expression persists in the cranial ectoderm and is upregulated in the presumptive olfactory placodes. By stages 11-12, expression declines in the neural tube, but not in the cranial ectoderm; in somites, expressed all along the rostral-caudal axis as well as in presomital mesenchyme caudal to the developing somites. Lens and otic placode expression first visible at stage 12, strongest at stages 13-16. Detected uniformly in ectoderm and mesenchyme of the limb primordia at stage 17. By stage 18, decrease of ectodermal, otic, lens and olfactory placode expression; expression appears in the epibranchial placodes. By stages 22-30, highest levels in the most distal mesoderm of the autopod, in the ventricular zone of the neural tube from the forebrain to the spinal cord, in the dermomyotomes and the tail buds.

-1- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).

-1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

-1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

-1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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EMBL: AF031831; AAB87969.1; .
 EMBL: AF224317; AAF61097.1; .
 InterPro: IPR000539; Frizzled.
 InterPro: IPR000024; Fz_domain.
 InterPro: IPR000832; GPCR_secretin.
 Pfam: PF01392; Fz; 1.
 Pfam: PF01534; Frizzled; 1.
 PRINTS: PR00489; FRIZZLED.
 SMART: SM00063; FRI; 1.
 PROSITE: PS00038; Fz; 1.
 PROSITE: PS0261; G-PROTEIN_RECEP_F2_4; 1.
 Multigene family: G-protein coupled receptor; Transmembrane;
 Developmental protein; Glycoprotein; Signal.
 SIGNAL 1 31 POTENTIAL.
 CHAIN 32 567
 DOMAIN 32 250 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 251 271 1 (POTENTIAL).
 DOMAIN 272 282 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 283 303 2 (POTENTIAL).
 DOMAIN 304 330 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 331 351 3 (POTENTIAL).
 DOMAIN 352 373 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 374 394 4 (POTENTIAL).
 DOMAIN 395 417 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 418 438 5 (POTENTIAL).
 DOMAIN 439 464 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 465 485 6 (POTENTIAL).
 DOMAIN 486 521 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 522 542 7 (POTENTIAL).
 DOMAIN 543 567 CYTOPLASMIC (POTENTIAL).
 DOMAIN 42 161 FZ.
 SITE 545 550 LYS-THR-X-X-X-TRP MOTIF.
 SITE 565 567 PDZ-BINDING.
 FT CARBOHYD 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 34 35 HE -> QD (IN REF. 2).
 FT CONFLICT 480 480 V -> L (IN REF. 2).
 SQ SEQUENCE 567 AA; 62811 MH; 3EFF0361FC699BC3 CRC64;
 16.3%; Score 306; DB 1; Length 567;

Best Local Similarity 39.2%; Pred. No. 4, 2e-18;
 Matches 62; Conservative 23; Mismatches 47; Indels 26; Gaps 5;

QY 12 WLHLA---LGVRCARCEA-----VRIPMCRHMPNITRMPNHLHST 50
 DB 14 WLGLAALLAALLGCAAAHEDKATSVDPHGFQCPISPLCTDIAYNQITLNLGHTN 73
 QY 51 QENAILAIEQYEELVDVNCASVLRFFFCAMYPATICTLEFLHDPKPKCKVCQRDDCEP 110
 DB 74 QEDAGLEVHGFYPLVKVQCSAELKFLCSMYAPVIV--LEQAIPCRSLCERARQCEA 131
 QY 111 LMKMYNHSWPESLACDELPLVYDRG-VCISPEAIVTDLP 147
 DB 132 LMKKGFQWPERLRCEFNFPVHGAGEICVQGN--TSDAP 167

RESULT 13
 FZD8_XENLA
 ID FZD8_XENLA STANDARD; PRT; 561 AA.
 AC O93274; Q9YI55;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (Xfz8).
 GN FZ8.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN 11
 RP SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY.
 RC TISSUE=Embryo;
 RX PubMed=9651509;
 RA Itoh K., Jacob J., Sokol S.Y.;
 RT 'Frizzled-8 is expressed in the Spemann organizer and plays a role in early morphogenesis.';
 RL Mech. Dev. 74:145-157(1998).
 RN 12
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=98301424; PubMed=9636083;
 RA Deardorff M.A., Tan C., Conrad L.J., Klein P.S.;
 RT 'Frizzled-8 is expressed in the Spemann organizer and plays a role in early morphogenesis.';
 RL Development 125:2687-2700(1998).
 CC -1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues. Activation by Wnt8, Wnt5A or Wnt3A induces expression of beta-catenin target genes. Displays an axis-inducing activity.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DEVELOPMENTAL STAGE: First expressed at high levels in the late blastula stages. At early gastrula, expressed in the deep cells of the Spemann organizer prior to involution of the dorsal blastopore lip. Detected in presumptive neuroectoderm as gastrulation proceeds. Becomes restricted to the anterior ectoderm by the end of gastrulation. At neurula stages, localized in the most anterior region of the embryo, mainly in the anterior ectoderm including telencephalic and cement gland regions.
 CC -1- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).
 CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED

more evident at stage 16. At stage 17, seen in the ectoderm and mesenchyme of the limb primordia. Detected at stage 20 in the lip of the optic cup, in the mesenchyme surrounding the eye, in the ectoderm overlying the lens and in the ectoderm caudal and ventral of the olfactory placodes. From stages 20-30, expressed in cartilage and in the dermomyotomes and migrating sclerotomal cells forming vertebrae.

CC -|- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).

CC -|- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

CC -|- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

CC -|- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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CC -----

DR EMBL: AF031830; AAB87968.1; -.

DR EMBL: AF224314; AAF61094.1; -.

DR InterPro: IPR000539; Frizzled.

DR InterPro: IPR000024; Fz_domain.

DR InterPro: IPR000832; GPCR_secretin.

DR Pfam: PF01392; Fz; 1.

DR Pfam: PF01392; Frizzled; 2.

DR SMART: SM00063; FRI; 1.

DR PROSITE: PS50038; FZ; 1.

DR PROSITE: PS50261; G-PROTEIN_RECEPTOR_F2_4; 1.

KW Multigene family; G-protein coupled receptor; Transmembrane;

KW Developmental protein; Glycoprotein; Signal.

FT SIGNAL 1 48 POTENTIAL.

FT -CHAIN 49 592 FRIZZLED 1.

FT DOMAIN 49 271 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 272 292 1 (POTENTIAL).

FT DOMAIN 293 303 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 304 324 2 (POTENTIAL).

FT -DOMAIN 325 351 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 352 372 3 (POTENTIAL).

FT DOMAIN 373 394 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 395 415 4 (POTENTIAL).

FT DOMAIN 416 438 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 439 459 5 (POTENTIAL).

FT DOMAIN 460 485 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 486 506 6 (POTENTIAL).

FT TRANSMEM 507 546 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 547 567 7 (POTENTIAL).

FT TRANSMEM 568 592 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 65 184 FZ.

FT SITE 570 575 LYS-THR-X-X-TRP MOTIF.

FT SITE 590 592 PDZ-BINDING.

FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 533 533 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 592 AA: 65490 MW: 933E76063CA6109D CRC64;

Query Match 16.3%; Score 305.5; DB 1; Length 592;

Best Local Similarity 42.9%; Pred. No. 4.9e-18;

Matches 57; Conservative 25; Mismatches 42; Indels 9; Gaps 3;

QY 16 ALVGRCAP-----CEAVRTPMCRHMPWNTRPNHLHSTQENALAIQYEELVDVNC 69

DB 56 ALSEGGISPDHGVCQIPISPLCTDIAYNQTIMPNLHGTNQDAGLEVHQFVPLVQVC 115

QY 70 SAVLRPFECAMYPACTLEFLHPDIPKPSVCORARDCEPLMKMYNHSWPESLACDELP 129

DB 116 SAELKFLCSMYAPVCTV--LEQALPCRSICERARQGCERALKMKFGQWPDTRCEKFP 173

QY 130 VYDRG-VCISPEA 141

DB 174 VHGAGELCVGQNA 186

RESULT 15

FZD8_MOUSE STANDARD; PRT; 685 AA.

AC FZD8_MOUSE 061091;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (mFz8).

GN FZD8.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96224032; PubMed=8626800;

RA Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;

RT "A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue polarity gene frizzled.";

RL J. Biol. Chem. 271:4468-4476(1996).

RN [2]

RP COUPLING TO BETA-CATENIN PATHWAY.

RX MEDLINE=99324245; PubMed=10395542;

RA Sheidahl L.C., Park M., Malbon C.C., Moon R.T.;

RT "Protein kinase C is differentially stimulated by Wnt and Frizzled homologs in a G-protein-dependent manner.";

RL Curr. Biol. 9:695-698(1999).

CC -|- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues. Activation by Wnt8 induces expression of beta-catenin target genes.

CC -|- SUBCELLULAR LOCATION: Integral membrane protein.

CC -|- TISSUE SPECIFICITY: Expressed in chondrocytes.

CC -|- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).

CC -|- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

CC -|- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

CC -|- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

CC -----

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CC -----

DR EMBL: U43321; AAC52433.1; -.

DR MGD; MG1:108460; Fzd8.

DR InterPro: IPR000539; Frizzled.

DR InterPro: IPR000024; Fz_domain.

DR InterPro: IPR000832; GPCR_secretin.

DR Pfam: PF01392; Fz; 1.

DR Pfam: PF01392; Frizzled; 1.

DR PRINTS; PR00489; FRIZZLED.

DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50261; G-PROTEIN_RECP_F2_4; 1.
KW Multigene family; G-protein coupled receptor; Transmembrane;
KW Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 27
FT CHAIN 28 685
FT DOMAIN 28 272
FT TRANSMEM 273 293
FT DOMAIN 294 309
FT TRANSMEM 310 330
FT DOMAIN 331 394
FT TRANSMEM 395 415
FT DOMAIN 416 437
FT TRANSMEM 438 458
FT DOMAIN 459 481
FT TRANSMEM 482 502
FT DOMAIN 503 530
FT TRANSMEM 531 551
FT DOMAIN 552 582
FT TRANSMEM 583 603
FT DOMAIN 604 685
FT DOMAIN 30 151
FT DOMAIN 168 173
FT DOMAIN 353 361
FT DOMAIN 640 654
FT SITE 606 611
FT SITE 683 685
FT CARBOHYD 49 49
FT CARBOHYD 152 152
FT CARBOHYD 473 473
SQ SEQUENCE 685 AA; 73215 MW; F333B49474411267 CRC64;

Query Match 16.2%; Score 305; DB 1; Length 685;
Best Local Similarity 39.5%; Pred. No. 6.4e-18;
Matches 58; Conservative 31; Mismatches 46; Indels 12; Gaps 5;
QY 4 SILVALCLHLALGVGA-----PCEAVRIPMCRHMPWNITRMPNHLHSTQENAILAI 58
Db 11 SLAALAV-LQRSSGAAASAKELACQETVPLCKGIGYNYTMPNQFNHDTODEAGLEV 69
QY 59 EOYEELVDVNCNAVLRFFFCAMYPICITLFLHDPIKPKCKSVQCRARDCEPLMKMYNHS 118
Db 70 HOFWPLVEIQSPDLKFFLCSMYTPIC-LEDYKKPLPPCRSVCRKAGCAPLMROYGFA 128
QY 119 WPESLACDELVPYDRGVCISPEAIVTD 145
Db 129 WPDRCORLP--EQG---NPDLCMD 150

Search completed: March 7, 2003, 11:24:18
Job time : 16 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 7, 2003, 11:20:59 ; Search time 35 Seconds
(without alignments)
2036.923 Million cell updates/sec

Title: US-09-909-775-2

Perfect score: 1879

Sequence: 1 MFLSILVALCLWLHLALGVR.....SPKNIKTRSAOKRTNPKRV 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 205047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1879	100.0	346	4	O14877
2	1746.5	92.9	351	11	Q921N6
3	1732	92.2	348	11	Q9JLS5
4	1720	91.5	348	11	Q35222
5	1485	79.0	303	11	Q924N2
6	1030	54.8	197	11	Q9JLS4
7	829	44.1	323	11	Q91W58
8	828	44.1	315	13	Q9IA95
9	822.5	43.8	319	13	P79993
10	816	43.4	318	13	P79936
11	799	42.5	315	13	Q9W6E0
12	791	42.1	148	11	Q912X9
13	673.5	35.8	213	13	Q9PTD9
14	621.5	33.1	261	11	O08570
15	512	27.2	130	6	Q95JB1
16	482.5	25.7	138	13	Q9PTN5

ALIGNMENTS

RESULT 1

ID	O14877	PRELIMINARY:	PRT;	346 AA.
AC	O14877;			
DC	O14877;			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	FrpHE.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=ENDOMETRIUM;			
RA	Abu-Jawdeh G.M., Comella N., Brown L.F., Tognazzi K., Kocher O.;			
RT	*frizzled related protein frpHE (Homo Sapiens).";			
RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF026692; AAC04617.1; -;			
DR	InterPro; IPR000024; Fz_domain.			
DR	InterPro; IPR001134; Netrin_C.			
DR	Pfam; PF01392; Fz; 1.			
DR	Pfam; PF01759; NTR; 1.			
DR	SMART; SM00063; FRI; 1.			
DR	PROSITE; PS50038; Fz; 1.			
SQ	SEQUENCE 346 AA; 39860 MW; 75D78D43E444CC2A CRC64;			

Query Match 100.0%; Score 1879; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 6.7e-164;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNTIRPNHLHHSTQENAILAIEQ	60
DB	1	MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNTIRPNHLHHSTQENAILAIEQ	60
QY	61	YEELVDVNCSAVLRRFFFCANYAPICLTLEFLHDPKPKSVCORARDDCEPLKKNYHNSWP	120
DB	61	YEELVDVNCSAVLRRFFFCANYAPICLTLEFLHDPKPKSVCORARDDCEPLKKNYHNSWP	120

QY 121 ESLACDELPHYDGVGVCISPEAIVTDLPEDVKWIDITPDMWQBRPLDVKRLSPDRCKC 180
 DB 121 ESLACDELPHYDGVGVCISPEAIVTDLPEDVKWIDITPDMWQBRPLDVKRLSPDRCKC 180
 QY 181 KVKVPTLATYLSKNYSYVIHAKIKAVORSGCNEVTTVDVKKEIFKSSSPIPTQVPLITN 240
 DB 181 KVKVPTLATYLSKNYSYVIHAKIKAVORSGCNEVTTVDVKKEIFKSSSPIPTQVPLITN 240
 QY 241 SSCQCCHILPHQDVLIMCYEWSRMMLLENCLVEKWRDQLSKRISQWEERLQQRRTVD 300
 DB 241 SSCQCCHILPHQDVLIMCYEWSRMMLLENCLVEKWRDQLSKRISQWEERLQQRRTVD 300
 QY 301 KKTAGTSSRNPCKGPKPPAPKSPKKNIKTRSAQKRTNPKRV 346
 DB 301 KKTAGTSSRNPCKGPKPPAPKSPKKNIKTRSAQKRTNPKRV 346
 RESULT 2
 Q9ZIN6 PRELIMINARY; PRT; 351 AA.
 AC Q9ZIN6;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE Secreted frizzled-related sequence protein 4.
 GN SFRP4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chang J.T., Esumi N., Moore K., Li Y., Zhang S., Chew C., Goodman B.,
 RA Ratner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
 RT "Cloning and characterization of a secreted frizzled-related protein
 RT that is expressed by the retinal pigment epithelium.";
 RL Hum. Mol. Genet. 0:0-0(1999).
 DR -EMBL; AF117709; AAD12306.1; -;
 DR MGD; MGI:892010; Sfrp4.
 DR InterPro: IPR000024; Fz_domain.
 DR Netrin_C.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF01759; NTR; 1.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; P550038; Fz; 1.
 SQ SEQUENCE 351 AA; 40342 MW; 6CB0B625920A54FE CRC64;

Query Match 92.9%; Score 1746.5; DB 11; Length 351;
 Best Local Similarity 92.5%; Pred. No. 9.2e-152;
 Matches 322; Conservative 9; Mismatches 14; Indels 3; Gaps 1;
 QY 1 MFLSILVALCLWLHLALGVGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
 DB 1 MLRSILVALCLWLRLALGVGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
 QY 61 YEELVDVNCSSVLRFFLCAMYPACTLEFLHDPKCKSVQCRARDCEPLMKMYNHSWP 120
 DB 61 YEELVDVNCSSVLRFFLCAMYPACTLEFLHDPKCKSVQCRARDCEPLMKMYNHSWP 120
 QY 121 ESLACDELPHYDGVGVCISPEAIVTDLPEDVKWIDITPDMWQBRPLDVKRLSPDRCKC 180
 DB 121 ESLACDELPHYDGVGVCISPEAIVTDLPEDVKWIDITPDMWQBRPLDVKRLSPDRCKC 180
 QY 181 KVKVPTLATYLSKNYSYVIHAKIKAVORSGCNEVTTVDVKKEIFKSSSPIPTQVPLITN 240
 DB 181 KVKVPTLATYLSKNYSYVIHAKIKAVORSGCNEVTTVDVKKEIFKSSSPIPTQVPLITN 240
 QY 241 SSCQCCHILPHQDVLIMCYEWSRMMLLENCLVEKWRDQLSKRISQWEERLQQRRTVD 300
 DB 241 SSCQCCHILPHQDVLIMCYEWSRMMLLENCLVEKWRDQLSKRISQWEERLQQRRTVD 300
 QY 301 KKTAGTSSRNPCKGPKPPAPKSPKKNIKTRSAQKRTNPKRV 346
 DB 301 KKTAGTSSRNPCKGPKPPAPKSPKKNIKTRSAQKRTNPKRV 346

DB 301 KKOIASRTSRTSRNPCKSGRPPAPKSPKKNIKARSAPKKSNLKK 348
 RESULT 3
 Q9JLS5 PRELIMINARY; PRT; 348 AA.
 AC Q9JLS5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Frizzled related protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FISHER;
 RX MEDLINE=21378144; PubMed=11485313;
 RA Yam J.W.P., Chan K.W., Wong V.K.W., Hsiao W.L.W.;
 RT "Transcriptional activity of the promoter region of rat frizzled-
 RT related protein gene.";
 RL Biochem. Biophys. Res. Commun. 286:94-100(2001).
 DR EMBL; AF140346; AAF66480.1; -;
 DR InterPro: IPR000024; Fz_domain.
 DR Netrin_C.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF01759; NTR; 1.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; P550038; Fz; 1.
 SQ SEQUENCE 348 AA; 39718 MW; 6CA7979D5A6C6A97 CRC64;
 Query Match 92.2%; Score 1732; DB 11; Length 348;
 Best Local Similarity 92.5%; Pred. No. 1.9e-150;
 Matches 319; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
 QY 1 MFLSILVALCLWLHLALGVGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
 DB 1 MLLSILVALCLWLRLALGVGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
 QY 61 YEELVDVNCSSVLRFFLCAMYPACTLEFLHDPKCKSVQCRARDCEPLMKMYNHSWP 120
 DB 61 YEELVDVNCSSVLRFFLCAMYPACTLEFLHDPKCKSVQCRARDCEPLMKMYNHSWP 120
 QY 121 ESLACDELPHYDGVGVCISPEAIVTDLPEDVKWIDITPDMWQBRPLDVKRLSPDRCKC 180
 DB 121 ESLACDELPHYDGVGVCISPEAIVTDLPEDVKWIDITPDMWQBRPLDVKRLSPDRCKC 180
 QY 181 KVKVPTLATYLSKNYSYVIHAKIKAVORSGCNEVTTVDVKKEIFKSSSPIPTQVPLITN 240
 DB 181 KVKVPTLATYLSKNYSYVIHAKIKAVORSGCNEVTTVDVKKEIFKSSSPIPTQVPLITN 240
 QY 241 SSCQCCHILPHQDVLIMCYEWSRMMLLENCLVEKWRDQLSKRISQWEERLQQRRTVD 300
 DB 241 SSCQCCHILPHQDVLIMCYEWSRMMLLENCLVEKWRDQLSKRISQWEERLQQRRTVD 300
 QY 301 KKTAGTSSRNPCKGPKPPAPKSPKKNIKTRSAQKRTNPKRV 345
 DB 301 KKOIASRTSRTSRNPCKSGRPPAPKSPKKNIKARSAPKKSNLKK 345
 RESULT 4
 Q9J222 PRELIMINARY; PRT; 348 AA.
 AC Q9J222;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Frizzled related protein frpAP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

DR	Pfam; PF01759; NTR; 1.
DR	PROSITE; PS50038; Fz; 1.
SQ	SEQUENCE 303 AA; 34507 MW; 8AB612A48933AAE1 CRC64;
	Query Match 79.0%; Score 1485; DB 11; Length 303;
	Best Local Similarity 96.1%; Pred. No. 6.7e-128;
	Matches 273; Conservative 2; Mismatches 9; Indels 0; Gaps
QY	1 MFLSILVALCLWLHLALGVGAPCEAVRIPMCRRHMPWNITRMPNHLHSHSQENAILAEIQ 60
Db	1 MLLSTLVALCLWLRLALGVGAPCEAVRIPMCRRHMPWNITRMPNHLHSHSQENAILAEIQ 60
QY	61 YEELVDVNCSAVLRFPPFCAMYPACTLEFLHDPIKPKCSVCQRARDCEPLMKMYNHSWP 120
Db	61 YEELVDVNCSSVLSFFFLCAMYPACTLEFLHDPIKPKCSVCQRARDCEPLMKMYNHSWP 120
QY	121 ESLACDELPPYDVGVCISPEAIVTDLDPEDVKWIDITPDMVMVQERPLDVCKRLSPORCKC 180
Db	121 ESLACDELPPYDVGVCISPEAIVTDLDPEDVKWIDITPDMVMVQERSFDADCKHLSPORCKC 180
QY	181 KVKPTLATYLSKNYSYVIHAKEIKAVQRSOCNEVTVVDVKEIFKSSSPIRTQVPLITN 240
Db	181 KVKPTLATYLSKNYSYVIHAKEIKAVQRSOCNEVTVVDVKEIFKSSSPIRTQVPLITN 240
QY	241 SSCOCPHLPDODVLINCYEWSRMMLLENCLVEKKWRDQLSKRS 284
Db	241 SSCOCPHLPDODVLINCYERRSRMMLLENCLVEKKWRDQLSKRS 284
RESULT 6	
Q9JLS4	PRELIMINARY; PRT; 197 AA.
ID	Q9JLS4
AC	Q9JLS4;
DT	01-OCT-2000 (TREMBLurel. 15, Created)
DF	01-OCT-2000 (TREMBLurel. 15, Last sequence update)
DT	01-JUN-2002 (TREMBLurel. 21, Last annotation update)
DE	Fizzled related protein (Fragment).
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
XC	NCBI_TaxID=10116;
RI	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=FISHER; TISSUE=LIVER;
RX	MEDLINE=21378144; Pubmed=11485313;
RA	Yam J.W.P., Chan K.W., Wong V.K.W., Hsiao W.L.W.;
RT	"Transcriptional activity of the promoter region of rat fizzled-
RL	related protein gene.";
DR	Biochem. Biophys. Res. Commun. 286:94-100(2001).
DR	EMBL; AF140347; AAF66481.1; -
DR	InterPro; IPR000024; Fz_domain.
DR	Pfam; PF01392; Fz; 1.
DR	SMART; SM00063; FRI; 1.
DR	PROSITE; PS50038; FZ; 1.
FT	NON_TER 197
SQ	SEQUENCE 197 AA; 22563 MW; CD4342B43B88692B CRC64;
	Query Match 54.8%; Score 1030; DB 11; Length 197;
	Best Local Similarity 94.9%; Pred. No. 1.8e-86;
	Matches 187; Conservative 1; Mismatches 9; Indels 0; Gaps
QY	1 MFLSILVALCLWLHLALGVGAPCEAVRIPMCRRHMPWNITRMPNHLHSHSQENAILAEIQ 60
Db	1 MLLSTLVALCLWLRLALGVGAPCEAVRIPMCRRHMPWNITRMPNHLHSHSQENAILAEIQ 60
QY	61 YEELVDVNCSAVLRFPPFCAMYPACTLEFLHDPIKPKCSVCQRARDCEPLMKMYNHSWP 120
Db	61 YEELVDVNCSSVLSFFFLCAMYPACTLEFLHDPIKPKCSVSQRARDCEPLMKMYNHSWP 120
QY	121 ESLACDELPPYDVGVCISPEAIVTDLDPEDVKWIDITPDMVMVQERPLDVCKRLSPORCKC 180
Db	121 ESLACDELPPYDVGVCISPEAIVTDLDPEDVKWIDITPDMVMVQERSFDADCKHLSPORCKC 180

QY 181 KVKKPTLATYLSKNYSY 197
 DB 181 KVKKPTLATYLSKNYSY 197

RESULT 7

Q91W58 PRELIMINARY; PRT; 323 AA.
 AC Q91W58;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Frizzled-related protein.
 GN FRZB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC016884; AAH16884.1; -.
 DR MGI: 892032; Frzb.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF01759; NTR; 1.
 DR PROSITE: PS50038; FZ; 1.
 SQ SEQUENCE 323 AA; 36039 MW; 3F1449B8CFC97740 CRC64;

Query Match 44.1%; Score 829; DB 11; Length 323;
 Best Local Similarity 51.1%; Pred. No. 8.2e-68;
 Matches 166; Conservative 49; Mismatches 76; Indels 34; Gaps 9;

QY 3 LSTLVALCLMLHALVGRGAPCEAVRIPMCRHMPNITRMPNHLHHSTQENAILAIEQYE 62
 DB 16 LLVLAALCL-LQVP-GAQAACAEVPRIPCKSLPWNMTKMPNHLHHSTQANAILAMEQFE 73
 QY 63 ELVDVNCASVLRFFFCAMYPACTLEFLHDPKPKSVQCARDDCEPLMKMYNHSWPES 122
 DB 74 GLGTGHCSPDLLFLFCAMYPACTIDFQHEPKPKSVQCARAGGCEPILIKYRHSWPES 133
 QY 123 LACDELPLYDRGVCISPEAIVT---DLPEVKKWIDITPDMVMQERPLDVCCKRLSPDRCK 178
 DB 134 LACDELPLYDRGVCISPEAIVTADGADFPMDSS-----TCHCRGASSERC 178
 QY 179 KCKVKPTLATYLSKNYSYVIAKIKAVQRSGCNEVTTVDVKEIFKSS-SPIPTQVPL 237
 DB 179 KCKPVRATQKTYPRNNYVIRAKVKKM-CHDVTAVVEVKEILKASLVNIPROTVNL 237
 QY 238 ITNSSCOCPHILPHQDVLMICY--EWSRMMLENCLEKVRDQSKRSIQWERLQ--- 292
 DB 238 YTTSGCLCPPLTAVNEEYVINGYEDEERSRLLLVEGSAEKWKDRLGKVKRNDKMLRHLG 297
 QY 293 -----EQRRVTQDKKKTAGRTSRNP 313
 DB 298 LGKTDASDSTQNK--SGRNSNRP 320

RESULT 8

Q91A95 PRELIMINARY; PRT; 315 AA.
 AC Q91A95;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Frzb.
 GN FRZB.
 OS Gallus gallus (Chicken)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Afchosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20123838; PubMed=10656762;
 RA Ladhari R.K., Church V.L., Allen S., Robson L., Abdelfattah A.,
 RA Brown N.A., Hattersley G., Rosen V., Luyten F.P., Dale L.,
 RA Francis-West P.H.;
 RT "Cloning and Expression of the Wnt Antagonists Sfrp-2 and Frzb during Chick Development.";
 RL Dev. Biol. 218:183-198(2000).
 DR EMBL: AF218057; AAF27643.1; -.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF01759; NTR; 1.
 DR SMART: SM00063; FRI; 1.
 DR PROSITE: PS50038; FZ; 1.
 SQ SEQUENCE 315 AA; 35003 MW; 6EBC58DB5335505D CRC64;

Query Match 44.1%; Score 828; DB 13; Length 315;
 Best Local Similarity 50.0%; Pred. No. 9.9e-68;
 Matches 162; Conservative 52; Mismatches 80; Indels 30; Gaps 6;

QY 4 SILVALCLMLHALVGRGAPCEAVRIPMCRHMPNITRMPNHLHHSTQENAILAIEQYE 63
 DB 7 ALALAALLLGRAPAGRAAACEVPRIPCKSLPWNMTKMPNHLHHSTQANAILAMEQFE 66
 QY 64 LVDVNCASVLRFFFCAMYPACTLEFLHDPKPKSVQCARDDCEPLMKMYNHSWPES 123
 DB 67 LGTNCSPDLLFLFCAMYPACTIDFQHEPKPKSVQCARAGGCEPVLIRYRHWPES 126
 QY 124 ACDELPLYDRGVCISPEAIVT---DLPEVKKWIDITPDMVMQERPLDVCCKRLSPDRCK 179
 DB 127 ACDELPLYDRGVCISPEAIVTAEADFPMDSN-----NGNCRGTGERCK 171
 QY 180 CKVKPTLATYLSKNYSYVIAKIKAVQRSGCNEVTTVDVKEIFKSS-SPIPTQVPLI 238
 DB 172 CKPIKATQKTYPRNNYVIRAKVKEV-KTKCHDVTAVVEVKEILKSSLVNIPKDTVNL 230
 QY 239 ITNSSCOCPHILPHQDVLMICY--EWSRMMLENCLEKVRDQSKRSIQWERLQ--- 296
 DB 231 TNSGCLCPPLTAVNEEYVINGYEDEERSRLLLVEGSAEKWKDRLGKVKRNDKMLRH--- 287
 QY 297 TVQDKKKTAGRTSRNSNPPKPKGP 320
 DB 288 ----LCKGKGPQSDSALKTGAP 307

RESULT 9

P79993 PRELIMINARY; PRT; 319 AA.
 ID P79993
 AC P79993;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Frzb precursor.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97236496; PubMed=9118219;
 RA Wang S., Krinks M., Lin K., Luyten F.P., Moos M. Jr.;
 RT "Frzb, a secreted protein expressed in the Spemann organizer, binds and inhibits Wnt-8.";
 RL Cell 88:757-766(1997).
 DR EMBL: U78598; AAC60114.1; -.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF01392; Fz; 1.

DR Pfam: PF01759; NTR; 1.
 DR SMART: SM00063; FRI; 1.
 DR PROSITE: PS50038; FZ; 1.
 KW SIGNAL.
 FT CHAIN 1 28 POTENTIAL.
 SQ SEQUENCE 319 AA; 36062 MW; 6E2F206E3DEC080 CRC64;
 Query Match 43.8%; Score 822.5; DB 13; Length 319;
 Best Local Similarity 50.2%; Pred. No. 3.2e-67;
 Matches 162; Conservative 49; Mismatches 73; Indels 39; Gaps 8;
 QY 22 APCEAVRIPMCRHMPNITRMPNHLHSTQENAILAEIOEYEEELVDVNCSAVLEFFFCAMY 81
 DB 29 ASCEVRIIPCKMSPNMTKMPNHLHSTQENAILAEIOEYEEELVDVNCSAVLEFFFCAMY 88
 QY 82 APICTLEFLHDPTKPKCSVCORARDDCEPLMKMYNHSWPSLACDELPPYDVGVCISPEA 141
 DB 89 APICTIDFQHEPIKPKCSVCERARAGEPILIKYRHTWPSLACEELPPYDVGVCISPEA 148
 QY 142 IVTDLPEDVKWIDITPDMVQERPLDVDCRCKKVKRPTLATYLSKNYSYV 198
 DB 149 IVT----VEQGTSDMPDF-----PMSNNGCGSTAGECHCKCKPKMASOKTYLKNYNYV 199
 QY 199 IHAKIKAVORSNGNEVTVDVKEIFKSS-SPIPTQVPLITNSSCQCCHILPHQDVLIM 257
 DB 200 IRAKVEV-KVRCHDATAIVEVKEILKSSLVNIPKDTVTLYTNSGCLCPOLVANEVYIM 258
 QY 258 CYE--WRSRMKLENCLEVKRDLKRSIQWEERLQEQRRTVQDKKKTAGRTSRNPPK 315
 DB 259 GYEDKERTLLVEGSLAEKVRDRLAKVKRWOKLRR-----PR 298
 QY 316 PKGPKPAPKSPKKNIKTRSAQ 338
 DB 299 KSKDPVAP----IPNKNNSRQAR 318
 RESULT 10
 P79936 PRELIMINARY; PRT; 318 AA.
 AC P79936;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE FZB-1.
 GN FZB-1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97236495; PubMed-9118218;
 RA Leyns L., Boumeester T., Kim S.H., Piccolo S., De Robertis E.M.;
 RT "Fzrb-1 is a secreted antagonist of Wnt signaling expressed in the
 RL Cell 88.747-756(1997).
 DR EMBL: U68059; AAC60113.1; -.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF01759; NTR; 1.
 DR SMART: SM00063; FRI; 1.
 DR PROSITE: PS50038; FZ; 1.
 SQ SEQUENCE 318 AA; 36005 MW; 5ED05E25F3C141DD CRC64;
 Query Match 43.4%; Score 816; DB 13; Length 318;
 Best Local Similarity 50.3%; Pred. No. 1.3e-66;
 Matches 161; Conservative 47; Mismatches 78; Indels 34; Gaps 7;
 QY 22 APCEAVRIPMCRHMPNITRMPNHLHSTQENAILAEIOEYEEELVDVNCSAVLEFFFCAMY 81
 DB 29 ASCEVRIIPCKMSPNMTKMPNHLHSTQENAILAEIOEYEEELVDVNCSAVLEFFFCAMY 88

DB 29 ASCEVRIIPCKMSPNMTKMPNHLHSTQENAILAEIOEYEEELVDVNCSAVLEFFFCAMY 88
 QY 82 APICTLEFLHDPTKPKCSVCORARDDCEPLMKMYNHSWPSLACDELPPYDVGVCISPEA 141
 DB 89 APICTIDFQHEPIKPKCSVCERARAGEPILIKYRHTWPSLACEELPPYDVGVCISPEA 148
 QY 142 IVTDLPEDVKWIDITPDMVQERPLDVDCRCKKVKRPTLATYLSKNYSYV 201
 DB 149 IVT----VEQGTSDMPDFSDMSNNGCGSGR---EHCKCKPKMATOKTYLKNYNYVIRA 201
 QY 202 KIKAVORSNGNEVTVDVKEIFKSS-SPIPTQVPLITNSSCQCCHILPHQDVLIMCYE 260
 DB 202 KIKVEV-KVRCHDATAIVEVKEILKSSLVNIPKDTVTLYTNSGCLCPOLVANEVYIMGYE 260
 QY 261 --WRSRMKLENCLEVKRDLKRSIQWEERLQEQRRTVQDKKKTAGRTSRNPPKPKG 318
 DB 261 DRETRHLLVEGSLAEKVRDRLAKVKRWOKLRR-----PRKSK 300
 QY 319 KPPAPKSPKKNIKTRSAQ 338
 DB 301 DPVAP---IPNKNNSRQAR 317
 RESULT 11
 Q9W6E0 PRELIMINARY; PRT; 315 AA.
 AC Q9W6E0;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE FZB-1.
 GN FZB1.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Furutani-Seiki M.;
 RT "Cloning of zebrafish fzb-1, antagonist of Wnt signaling."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinya M., Driever W., Furutani-Seiki M.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: ARL16853; AAD22462.1; -.
 DR ZFIN: ZDB-GENE-990715-1; fzb1.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF01759; NTR; 1.
 DR SMART: SM00063; FRI; 1.
 DR PROSITE: PS50038; FZ; 1.
 DR PROSITE: PS50038; FZ; 1.
 SQ SEQUENCE 315 AA; 36031 MW; 0F23DFF09F9B9414 CRC64;
 Query Match 42.5%; Score 799; DB 13; Length 315;
 Best Local Similarity 50.2%; Pred. No. 4.5e-65;
 Matches 155; Conservative 55; Mismatches 77; Indels 22; Gaps 9;
 QY 1 MFLSILVALCLWLHLAGVIRGAPCEAVRIPMCRHMPNITRMPNHLHSTQENAILAEIOE 60
 DB 9 MFICVLAFACL-LEIPRGTAASCEPIRIPMCKSMSPNMTKMPNHLHSTQENAILAEIOE 67
 QY 61 YEELVDVNCSAVLEFFFCAMYAPICTLEFLHDPTKPKCSVCORARDDCEPLMKMYNHSW 120
 DB 68 FEGLLTQCSADLLFFLCAMYAPICTIDFQHEPIKPKCSVCERAKCKGCEVPMRYNHTWP 127
 QY 121 ESLACDELPPYDVGVCISPEAIV-TDLPEVVKWIDI-----TPDMVQERPLD---VD 169
 DB 128 ESLACDELPPYDVGVCISPEAIVKAEGPDNSYODPAKCNPEGNPDF-----PMSINTN 182
 QY 170 CKRLSPDRCKCKVKPTLATYLSKNYSYVIAKIKAVORSNGNEVTVDVVKEIFKSS-S 228

Search completed: March 7, 2003, 11:24:59
Job time : 38 secs

infusion vs. oral → evaluation
scope

Variation between maximum.

PP-4

Sept. 2000 bovine

are all maximum. described

W.D. on claim 5.